

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 13:52:13 ; Search time 7671 Seconds
(without alignments)
4649.073 Million cell updates/sec

Title: US-10-075-105C-1

Perfect score: 736

Sequence: 1 ggatccagcgtgtctctcc.....ggagaggacacgtggtatcc 736

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hcg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sta.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	554	75.3	661	6 I06305	I06305 Sequence 34
2	554	75.3	661	6 I07318	I07318 Sequence 30
3	554	75.3	2107	6 AR229556	AR229556 Sequence
4	554	75.3	2122	6 AR229554	AR229554 Sequence
5	554	75.3	2436	6 AR229557	AR229557 Sequence
6	554	75.3	3469	6 AR271023	AR271023 Sequence
7	554	75.3	3754	6 AR271019	AR271019 Sequence
8	554	75.3	8012	6 AR143709	AR143709 Sequence
9	554	75.3	8012	6 BD008400	BD008400 Sequence
10	554	75.3	8349	6 AR260588	AR260588 Sequence
11	554	75.3	8418	6 AR143713	AR143713 Sequence
12	554	75.3	8418	6 BD008404	BD008404 Sequence
13	554	75.3	8798	6 AR143712	AR143712 Sequence
14	554	75.3	8798	6 BD008403	BD008403 Sequence
15	552.4	75.1	661	6 BD013916	BD013916 Sequence
16	551.4	74.9	1030	6 AR003011	AR003011 Sequence
17	551.4	74.9	5796	6 AX151106	AX151106 Sequence
18	551.4	74.9	5897	6 BD132716	BD132716 Sequence
19	551.4	74.9	5897	6 AR209019	AR209019 Sequence

20	551.4	74.9	5897	6	AR482088	AR482088 Sequence
c 21	551.4	74.9	9361	6	BD251965	BD251965 Artificialia
c 22	551.4	74.9	10629	6	BD251966	BD251966 Artificialia
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25	550.4	74.8	9335	6	AR482081	AR482081 Sequence
26	550	74.7	10249	6	AR260586	AR260586 Sequence
27	550	74.7	10339	6	AR260585	AR260585 Sequence
28	548.4	74.5	10160	6	BD132698	BD132698 Regulator
29	548.4	74.5	10160	6	AR209001	AR209001 Sequence
30	548.4	74.5	10160	6	AR482070	AR482070 Sequence
31	548.4	74.5	11784	6	BD132699	BD132699 Regulator
32	548.4	74.5	11784	6	AR209002	AR209002 Sequence
33	548.4	74.5	11784	6	AR482071	AR482071 Sequence
34	548.4	74.5	11991	6	BD132700	BD132700 Regulator
35	548.4	74.5	11991	6	AR209003	AR209003 Sequence
36	548.4	74.5	11991	6	AR482072	AR482072 Sequence
37	543.6	73.9	4149	6	AR271018	AR271018 Sequence
38	534.6	72.6	5767	6	AX275254	AX275254 Sequence
39	534.6	72.6	14446	6	AX275255	AX275255 Sequence
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c 41	526	71.5	8626	12	CVU10488	U10488 Binary clon
c 42	526	71.5	8731	12	CVU10463	U10463 Binary clon
c 43	526	71.5	8731	12	CVU10491	U10491 Binary clon
c 44	526	71.5	8909	12	CVU10458	U10458 Binary clon
c 45	526	71.5	8909	12	CVU10487	U10487 Binary clon

ALIGNMENTS

RESULT 1
LOCUS I06305 661 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 34 from Patent EP 0289479.
ACCESSION I06305
VERSION I06305.1 GI:590686
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 661)
AUTHORS Fischhoff,D.A., Fuchs,R.L., McPherson,S.A., Lavrik,P.B. and Perlak,F.J.
TITLE Insect-resistant plants
JOURNAL Patent: Ep 0289479-A2 34 02-NOV-1988;
FEATURES Location/Qualifiers
source
1..661
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN	Query Match	75.3%	Score 554;	DB 6;	Length 661;
	Best Local Similarity	94.5%	Pred. No. 2.5e-163;		
	Matches 586;	Conservative 0;	Mismatches 30;	Indels 4;	Gaps 1;
Qy	116	TCTCAGTGAGACTTTTCAACAAAGGGTAAATATCGGAAACCTCTCGGATTCATTGCC	175		
Db	20	TCCGATGTGAGACTTTTCAACAAAGGGTAAATATCGGAAACCTCTCTCGGATTCATTGCC	79		
Qy	176	CAGTATCTGTCTACTTCATCAAAAGGACAGTAGAAAAGGAGTGGGACCTACAAATGCC	235		
Db	80	CAGTATCTGTCTACTTTTGTGAAGATAGTGGAAAAGGAGTGGTCTCTACAAATGCC	139		
Qy	236	ATCATTCGGATAAGGAAAGGCTATCGTTCAGATGCTCTGCCGACAGTGGTCCCAAG	295		
Db	140	ATCATTCGGATAAGGAAAGGCTATCGTTCAGATGCTCTGCCGACAGTGGTCCCAAG	199		
Qy	296	ATGACCCCCCACCACCGAGGAGCATCGTGGAAAAGACGTTTCCAAACACGCTTTCAA	355		
Db	200	ATGGACCCCCCACCACCGAGGAGCATCGTGGAAAAGACGTTTCCAAACACGCTTTCAA	259		
Qy	356	AGCAAGTGGATTGATGTGAT-----TGCAGTGAGACTTTTCAACAAAGGGTAAATATCGGGA	411		

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Db 260 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGTAATATCCGA 319
Qy 412 AACCTCTCGGATTCCTTGGCCAGCTATCTGTCACTTCAATAAGAGCAGTAGAAAAG 471
Db 320 AACCTCTCGGATTCCTTGGCCAGCTATCTGTCACTTATGTGAAGATAGTGGAAG 379
Qy 472 GAAGGTGGCACTACAAATGCCATCATTTGGGATAAAGGAAGGCTATCGTTCAAGATGCC 531
Db 380 GAAGGTGGCTTCTTCAAAATGCCATCATTTGGGATAAAGGAAGGCTATCGTTGAAGATGCC 439
Qy 532 TCTGCCGACAGTGGTCCCAAGATGGATTCGATTAAGGAAGGCTATCGTTCAAGATGCC 531
Db 380 GAAGGTGGCTTCTTCAAAATGCCATCATTTGGGATAAAGGAAGGCTATCGTTGAAGATGCC 439
Qy 532 TCTGCCGACAGTGGTCCCAAGATGGATTCGATTAAGGAAGGCTATCGTTCAAGATGCC 531
Db 440 TCTGCCGACAGTGGTCCCAAGATGGATTCGATTAAGGAAGGCTATCGTTGAAGATGCC 499
Qy 592 GACGTTTCCAAACCAAGTGGTCCCAAGATGGATTCGATTAAGGAAGGCTATCGTTCAAGATGCC 651
Db 440 TCTGCCGACAGTGGTCCCAAGATGGATTCGATTAAGGAAGGCTATCGTTGAAGATGCC 499
Qy 592 GACGTTTCCAAACCAAGTGGTCCCAAGATGGATTCGATTAAGGAAGGCTATCGTTCAAGATGCC 651
Db 500 GACGTTTCCAAACCAAGTGGTCCCAAGATGGATTCGATTAAGGAAGGCTATCGTTCAAGATGCC 559
Qy 652 GATGACGACAAATCCCACTATCTTCCGCAAGACCTTCTCTATATAAGGAAGTTCATTT 711
Db 560 GATGACGACAAATCCCACTATCTTCCGCAAGACCTTCTCTATATAAGGAAGTTCATTT 619
Qy 712 CATTTGGAGAGGACACGCTG 731
Db 620 CATTTGGAGAGGACACGCTG 639

RESULT 2
I07318
LOCUS I07318 661 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 30 from Patent EP 0339009.
ACCESSION I07318
VERSION I07318.1 GI:589916
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 661)
AUTHORS Fuchs,R.L., Kishore,G.M. and MacIntosh,S.C.
TITLE Method for improving the efficacy of insect toxins
JOURNAL Patent: EP 0339009-A2 30 25-OCT-1989;
FEATURES Location/Qualifiers
source 1. .661
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 75.3%; Score 554; DB 6; Length 661;
Best Local Similarity 94.5%; Pred. No. 2.5e-163;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTGCAGTGAGACTTTTCAACAAAGGTAATATCGGGAACCTCTCTCGGATTCGATGCC 175
Db 20 TCCGATGTGAGACTTTTCAACAAAGGTAATATCGGGAACCTCTCTCGGATTCGATGCC 79
Qy 176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAGTGCGACCTACAAATGCC 235
Db 80 CAGCTATCTGTCACTTTTATGTGAAGATAGTGGAAAAGGAGTGCGCTCTACAAATGCC 139
Qy 236 ATCATTTGCGATAAAGGAAGGCTATCGTTCAAGATGCTCTCGCGACAGTGGTCCCAAG 295
Db 140 ATCATTTGCGATAAAGGAAGGCTATCGTTGAAGATGCTCTCGCGACAGTGGTCCCAAG 199
Qy 296 ATGACACCCCAACCCACAGAGGACATCGTGGAAAAGAGAGCTTCGAAACACGCTCTTCAA 355
Db 200 ATGACACCCCAACCCACAGAGGACATCGTGGAAAAGAGAGCTTCGAAACACGCTCTTCAA 259
Qy 356 AGCAAGTGGATTTGATGTGAT-----TGCACTGTGAGACTTTTCAACAAAGGTAATATCGGA 411
Db 260 AGCAAGTGGATTTGATGTGATGCGGATGCGGATTTTCAACAAAGGTAATATCGGA 319
Qy 412 AACCTCTCGGATTCCTTGGCCAGCTATCTGTCACTTCAATAAGGACAGTAGAAAAG 471
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Db 320 AACCTCTCGGATTCCTTGGCCAGCTATCTGTCACTTTATTTGTGAAGATAGTGGAAG 379
Qy 472 GAAGGTGGCACTTACAAATGCCATCATTTGCGATAAAGGAAGGCTATCGTTCAAGATGCC 531
Db 380 GAAGGTGGCTTCTTACAAATGCCATCATTTGCGATAAAGGAAGGCTATCGTTGAAGATGCC 439
Qy 532 TCTGCCGACAGTGGTCCCAAGATGGATTCGATTAAGGAAGGCTATCGTTGAAGATGCC 591
Db 440 TCTGCCGACAGTGGTCCCAAGATGGATTCGATTAAGGAAGGCTATCGTTGAAGATGCC 499
Qy 592 GACGTTTCCAAACCAAGTGGTCCCAAGATGGATTCGATTAAGGAAGGCTATCGTTCAAGATGCC 651
Db 500 GACGTTTCCAAACCAAGTGGTCCCAAGATGGATTCGATTAAGGAAGGCTATCGTTCAAGATGCC 559
Qy 652 GATGACGACAAATCCCACTATCTTCCGCAAGACCTTCTCTATATAAGGAAGTTCATTT 711
Db 560 GATGACGACAAATCCCACTATCTTCCGCAAGACCTTCTCTATATAAGGAAGTTCATTT 619
Qy 712 CATTTGGAGAGGACACGCTG 731
Db 620 CATTTGGAGAGGACACGCTG 639

RESULT 3
AR229556
LOCUS AR229556 2107 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 29 from patent US 6448476.
ACCESSION AR229556
VERSION AR229556.1 GI:27269172
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2107)
AUTHORS Barry,G.F.
TITLE AMPA-N-acetyltransferase
JOURNAL Patent: US 6448476-A 29 10-SEP-2002;
FEATURES Location/Qualifiers
source 1. .2107
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/mol_type="genomic DNA"

ORIGIN
Query Match 75.3%; Score 554; DB 6; Length 2107;
Best Local Similarity 94.5%; Pred. No. 2.7e-163;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTGCAGTGAGACTTTTCAACAAAGGTAATATCGGGAACCTCTCTCGGATTCGATGCC 175
Db 28 TCCGATGTGAGACTTTTCAACAAAGGTAATATCGGGAACCTCTCTCGGATTCGATGCC 87
Qy 176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAGTGCGACCTACAAATGCC 235
Db 88 CAGCTATCTGTCACTTTTATGTGAAGATAGTGGAAAAGGAGTGCGCTCTACAAATGCC 147
Qy 236 ATCATTTGCGATAAAGGAAGGCTATCGTTCAAGATGCTCTCGCGACAGTGGTCCCAAG 295
Db 148 ATCATTTGCGATAAAGGAAGGCTATCGTTGAAGATGCTCTCGCGACAGTGGTCCCAAG 207
Qy 296 ATGACACCCCAACCCACAGAGGACATCGTGGAAAAGAGAGCTTCGAAACACGCTCTTCAA 355
Db 208 ATGACACCCCAACCCACAGAGGACATCGTGGAAAAGAGAGCTTCGAAACACGCTCTTCAA 267
Qy 356 AGCAAGTGGATTTGATGTGAT-----TGCACTGTGAGACTTTTCAACAAAGGTAATATCGGA 411
Db 268 AGCAAGTGGATTTGATGTGATGCGGATGCGGATTTTCAACAAAGGTAATATCGGA 327
Qy 412 AACCTCTCGGATTCCTTGGCCAGCTATCTGTCACTTCAATAAGGACAGTAGAAAAG 471
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Qy 472 GAAGTGGCAGCTACAAATGCCATCAATTCGATGAAGGAAAGGCTATCGTTCAAGATGCC 531
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Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCACCACGAGGAGCATCGTCGAAAGAAAGAA 591
Db 448 TCTGCCGACAGTGGTCCCAAGATGGACCCACCACGAGGAGCATCGTCGAAAGAAAGAA 507
Qy 592 GACGTTCCAAACACAGTCTTCAAGCAAGTGAATGATGATATCTCCACATGACGTAAGG 651
Db 508 GACGTTCCAAACACAGTCTTCAAGCAAGTGAATGATGATATCTCCACATGACGTAAGG 567
Qy 652 GATGACGACAAATCCCACTATCTTCCGAAAGCCCTTCTCTATATAAGGAAGTTCATTT 711
Db 568 GATGACGACAAATCCCACTATCTTCCGAAAGCCCTTCTCTATATAAGGAAGTTCATTT 627
Qy 712 CATTTGGAGAGGACACGCTG 731
Db 628 CATTTGGAGAGGACACGCTG 647

RESULT 4
AR229554
LOCUS AR229554 2122 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 25 from patent US 6448476.
ACCESSION AR229554
VERSION AR229554.1 GI:27269170
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 2122)
AUTHORS Barry.G.F.
TITLE Plants and plant cells transformation to express an
JOURNAL AMPA-N-acetyltransferase
FEATURES
Location/Qualifiers
1..2122
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 75.3%; Score 554; DB 6; Length 2122;
Best Local Similarity 94.5%; Pred. No. 2.7e-163;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
Db 8 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 67
Qy 176 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAGGAGGTGGCACCTACAAATGCC 235
Db 68 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAGGAGGTGGCTCTCAAAATGCC 127
Qy 236 ATCATTTGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGTGGTCCCAAG 295
Db 128 ATCATTTGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGTGGTCCCAAG 187
Qy 296 ATGACCCCAACCCACGAGGAGCATCGTGGAAAAGAGAGCTTCCAAACACGCTTCAA 355
Db 188 ATGACCCCAACCCACGAGGAGCATCGTGGAAAAGAGAGCTTCCAAACACGCTTCAA 247
Qy 356 AGCAAGTGGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 411
Db 248 AGCAAGTGGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 307
Qy 412 AACCTCTCGGATTCATTCGCGGAGCTATCTGTCACTTTCATCAAAAGGAGTGAAGAAAG 471
Db 308 AACCTCTCGGATTCATTCGCGGAGCTATCTGTCACTTTCATCAAAAGGAGTGAAGAAAG 367
Qy 472 GAAGTGGCAGCTACAAATGCCATTCGATGAAGGAGGCTATCGTTCAAGATGCC 531
Db 368 GAAGTGGCTCCTACAAATGCCATTCGATGAAGGAGGCTATCGTTGAAGATGCC 427
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Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCACCACGAGGAGCATCGTGGAAAGAAAGAA 591
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Qy 592 GACGTTCCAAACACAGTCTTCAAGCAAGTGAATGATGATATCTCCACATGACGTAAGG 651
Db 488 GACGTTCCAAACACAGTCTTCAAGCAAGTGAATGATGATATCTCCACATGACGTAAGG 547
Qy 652 GATGACGACAAATCCCACTATCTTCCGAAAGCCCTTCTCTATATAAGGAAGTTCATTT 711
Db 548 GATGACGACAAATCCCACTATCTTCCGAAAGCCCTTCTCTATATAAGGAAGTTCATTT 607
Qy 712 CATTTGGAGAGGACACGCTG 731
Db 608 CATTTGGAGAGGACACGCTG 627

RESULT 5
AR229557
LOCUS AR229557 2436 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 31 from patent US 6448476.
ACCESSION AR229557
VERSION AR229557.1 GI:27269173
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 2436)
AUTHORS Barry.G.F.
TITLE Plants and plant cells transformation to express an
JOURNAL AMPA-N-acetyltransferase
FEATURES
Location/Qualifiers
1..2436
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ORIGIN
Query Match 75.3%; Score 554; DB 6; Length 2436;
Best Local Similarity 94.5%; Pred. No. 2.7e-163;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
Db 28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 87
Qy 176 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAGGAGGTGGCACCTACAAATGCC 235
Db 88 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAGGAGGTGGCTCTCAAAATGCC 147
Qy 236 ATCATTTGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGTGGTCCCAAG 295
Db 148 ATCATTTGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGTGGTCCCAAG 207
Qy 296 ATGACCCCAACCCACGAGGAGCATCGTGGAAAAGAGAGCTTCCAAACACGCTTCAA 355
Db 208 ATGACCCCAACCCACGAGGAGCATCGTGGAAAAGAGAGCTTCCAAACACGCTTCAA 267
Qy 356 AGCAAGTGGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 411
Db 268 AGCAAGTGGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 327
Qy 412 AACCTCTCGGATTCATTCGCGGAGCTATCTGTCACTTTCATCAAAAGGAGTGAAGAAAG 471
Db 328 AACCTCTCGGATTCATTCGCGGAGCTATCTGTCACTTTCATCAAAAGGAGTGAAGAAAG 387
Qy 472 GAAGTGGCAGCTACAAATGCCATTCGATGAAGGAGGCTATCGTTCAAGATGCC 531
Db 388 GAAGTGGCTCCTACAAATGCCATTCGATGAAGGAGGCTATCGTTGAAGATGCC 447
Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCACCACGAGGAGCATCGTGGAAAGAAAGAA 591
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Db 448 TCTGCCGACAGTGGTCCAAAAGATGGACCCACCACGAGGAGCATCGTGGAAAAAGAA 507
Qy 592 GAGGTTCCAAACCAGCTTTCAAGCAAGTGGATGATGATATCTCCACTGACGTAAGG 651
Db 508 GAGGTTCCAAACCAGCTTTCAAGCAAGTGGATGATGATATCTCCACTGACGTAAGG 567
Qy 652 GATGACGACAAATCCCACTATCCTTCGCAAGACCTTCCTCTATATAGGAAGTTCATTT 711
Db 568 GATGACGACAAATCCCACTATCCTTCGCAAGACCTTCCTCTATATAGGAAGTTCATTT 627
Qy 712 CATTTGGAGGACACGCTG 731
Db 628 CATTTGGAGGACACGCTG 647
RESULT 6
LOCUS AR271023 3469 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 23 from patent US 6501009.
ACCESSION AR271023
VERSION AR271023.1 GI:29702289
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3469)
AUTHORS Romano, C.P.
TITLE Expression of Cry3B insecticidal protein in plants
JOURNAL Patent: US 6501009-A 23 31-DEC-2002;
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/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 75.3%; Score 554; DB 6; Length 3469;
Best Local Similarity 94.5%; Pred. No. 2.7e-163;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
Qy 116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCGATTGCC 175
Db 28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCGATTGCC 87
Qy 176 CAGCTATCTGTCACTTTCATCAAAAGGACGTAGAAAAGGAGTGGACCTACAAATGCC 235
Db 88 CAGCTATCTGTCACTTTCATCAAAAGGACGTAGAAAAGGAGTGGCTCTACAAATGCC 147
Qy 236 ATCAATTCGGATAAAGGAAGGCTATCGTTCAAGATCGCTCTGCGACAGTGGTCCCAAG 295
Db 148 ATCAATTCGGATAAAGGAAGGACCATCGTTGAAGATGCTCTGCGACAGTGGTCCCAAG 207
Qy 296 ATGGACCCCAACCCACGAGAGCATCGTGGAAAAGAGACGTTTCCAAACCAAGTTCCTCA 355
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Qy 356 AGCAAGTGGATTGATGTGAT- - - - -TGCAGTGGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db 268 AGCAAGTGGATTGATGTGATGTGCGGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 327
Qy 412 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 471
Db 328 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTTATTTGTAAGATAGTGGAAAAG 387
Qy 472 GAAGTGGGACCTTCAATTCGCCAGCTATTCGATATAAGGAAGGCTATCGTTCAAGATGCC 531
Db 328 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTTATTTGTAAGATAGTGGAAAAG 387
Qy 472 GAAGTGGGACCTTCAATTCGCCAGCTATTCGATATAAGGAAGGCTATCGTTCAAGATGCC 531
Db 388 GAAGTGGGCTCTCAATTCGCCAGCTATTCGATATAAGGAAGGCTATCGTTCAAGATGCC 447
Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAA 591
Db 448 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAA 507
Qy 592 GAGGTTCCAAACCAGCTTTCAAGCAAGTGGATGATGATATCTCCACTGACGTAAGG 651
Db 448 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAA 507
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Db 508 GAGGTTCCAAACCAGCTTTCAAGCAAGTGGATGATGATATCTCCACTGACGTAAGG 567
Qy 652 GATGACGACAAATCCCACTATCCTTCGCAAGACCTTCCTCTATATAGGAAGTTCATTT 711
Db 568 GATGACGACAAATCCCACTATCCTTCGCAAGACCTTCCTCTATATAGGAAGTTCATTT 627
Qy 712 CATTTGGAGGACACGCTG 731
Db 628 CATTTGGAGGACACGCTG 647
RESULT 7
LOCUS AR271019 3754 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 15 from patent US 6501009.
ACCESSION AR271019
VERSION AR271019.1 GI:29702285
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3754)
AUTHORS Romano, C.P.
TITLE Expression of Cry3B insecticidal protein in plants
JOURNAL Patent: US 6501009-A 15 31-DEC-2002;
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/organism="unknown"
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ORIGIN
Query Match 75.3%; Score 554; DB 6; Length 3754;
Best Local Similarity 94.5%; Pred. No. 2.7e-163;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
Qy 116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCGATTGCC 175
Db 28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCTCGGATTCGATTGCC 87
Qy 176 CAGCTATCTGTCACTTTCATCAAAAGGACGTAGAAAAGGAGTGGACCTACAAATGCC 235
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Qy 236 ATCAATTCGGATAAAGGAAGGCTATCGTTCAAGATCGCTCTGCGACAGTGGTCCCAAG 295
Db 148 ATCAATTCGGATAAAGGAAGGACCATCGTTGAAGATGCTCTGCGACAGTGGTCCCAAG 207
Qy 296 ATGGACCCCAACCCACGAGGAGCATCGTGGAAAAGAGACGTTTCCAAACCAAGTTCCTCA 355
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Qy 356 AGCAAGTGGATTGATGTGAT- - - - -TGCAGTGGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db 268 AGCAAGTGGATTGATGTGATGTGCGGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 327
Qy 412 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 471
Db 328 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTTATTTGTAAGATAGTGGAAAAG 387
Qy 472 GAAGTGGGACCTTCAATTCGCCAGCTATTCGATATAAGGAAGGCTATCGTTCAAGATGCC 531
Db 388 GAAGTGGGCTCTCAATTCGCCAGCTATTCGATATAAGGAAGGCTATCGTTCAAGATGCC 447
Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAA 591
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Qy 592 GAGGTTCCAAACCAGCTTTCAAGCAAGTGGATGATGATATCTCCACTGACGTAAGG 651
Db 508 GAGGTTCCAAACCAGCTTTCAAGCAAGTGGATGATGATATCTCCACTGACGTAAGG 567
Qy 652 GATGACGACAAATCCCACTATCCTTCGCAAGACCTTCCTCTATATAGGAAGTTCATTT 711


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Qy 592 GACGTTCAACCCAGTCTTCAAGCAAGTGATGTGATATCTCCTCACTGACGTAAGG 651
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Db 3524 GACGTTCAACCCAGTCTTCAAGCAAGTGATGTGATATCTCCTCACTGACGTAAGG 3583
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Qy 652 GATGACGACAATCCCACTATCTCTTCCGACAGACCTTCTCTATATATAAGGAAGTTCATTT 711
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Qy 712 CATTGGAGAGGACACGCTG 731
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Db 3644 CATTGGAGAGGACACGCTG 3663
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RESULT 10
LOCUS AR260588 8349 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 16 from patent US 6489542.
ACCESSION AR260588
VERSION AR260588.1 GI:27311143
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 8349)
AUTHORS Corbin,D.R. and Romano,C.P.
TITLE Methods for transforming plants to express Cry2Ab
JOURNAL delta-endotoxin targeted to the plastids
FEATURES
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Best Local Similarity 94.5%; Pred. No. 2.8e-163;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
Qy 116 TCTGCACTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCCTCGGATTCATTTGCC 175
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Db 1807 TCGATGTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCCTCGGATTCATTTGCC 1866
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Qy 176 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAGGAGTGGCACCACATCAAAATGCC 235
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Db 1867 CAGCTATCTGTCACTTATTTGTGAAGATAGTGGAAAGGAGTGGCTCTTCAAAATGCC 1926
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|
Db 1927 ATCATTCGGATAAAGGAAAGGCTATCGTTGAAGATGCTCTGCGACAGTGGTCCCAAAG 1986
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Qy 296 ATGACCCCCACCCACGAGGAGCATCGTGGAAAAGAGACGTTCCAAACCACTCTTCAA 355
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Db 1987 ATGACCCCCACCCACGAGGAGCATCGTGGAAAAGAGACGTTCCAAACCACTCTTCAA 2046
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Qy 356 AGCAAGTGGATTGATGTGAT- ---TGCAGTGAGACTTTTCAACAAGGGTAATATCGGGA 411
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|
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Db 2107 AACCTCTCGGATTCATTTGCCAGGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 2166
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Qy 472 GAAGTGGACCTTACAAATGCCATCATTTGGGATAAAGGAAGGCTATCGTTCAAGATGCC 531
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Db 2167 GAAGTGGCTTCTTCAAAATGCCATCATTTGGGATAAAGGAAGGCTATCGTTGAAGATGCC 2226
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Qy 532 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAA 591
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Db 2407 CATTGGAGAGGACACGCTG 2426
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RESULT 11
LOCUS AR143713 8418 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 5 from patent US 6204436.
ACCESSION AR143713
VERSION AR143713.1 GI:15104999
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 8418)
AUTHORS Mannerloef,M., Tenning,P.Peter. and Steen,P.
TITLE Transgenic plants
JOURNAL Patent: US 6204436-A 5 20-MAR-2001;
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Query Match 75.3%; Score 554; DB 6; Length 8418;
Best Local Similarity 94.5%; Pred. No. 2.8e-163;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
Qy 116 TCTGCACTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCCTCGGATTCATTTGCC 175
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Db 3023 TCGATGTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCCTCGGATTCATTTGCC 3082
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Qy 176 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAGGAGTGGCACCACATCAAAATGCC 235
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Db 3083 CAGCTATCTGTCACTTATTTGTGAAGATAGTGGAAAAGGAGTGGCTCTTCAAAATGCC 3142
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Qy 236 ATCATTCGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGACAGTGGTCCCAAAG 295
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Db 3143 ATCATTCGGATAAAGGAAAGGCTATCGTTGAAGATGCTCTGCGACAGTGGTCCCAAAG 3202
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Qy 296 ATGACCCCCACCCACGAGGAGCATCGTGGAAAAGAGACGTTCCAAACCACTCTTCAA 355
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Qy 356 AGCAAGTGGATTGATGTGAT- ---TGCAGTGAGACTTTTCAACAAGGGTAATATCGGGA 411
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Db 3263 AGCAAGTGGATTGATGTGATGCTCGGATGTGAGACTTTTCAACAAGGGTAATATCGGGA 3322
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Qy 412 AACCTCTCGGATTCATTTGCCAGGCTATCTGTCACTTCAATCAAAAGGACAGTAGAAAAG 471
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Db 3323 AACCTCTCGGATTCATTTGCCAGGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 3382
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Qy 472 GAAGTGGACCTTACAAATGCCATCATTTGGGATAAAGGAAGGCTATCGTTCAAGATGCC 531
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Db 3383 GAAGTGGCTCTTCAAAATGCCATCATTTGGGATAAAGGAAGGCTATCGTTGAAGATGCC 3442
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Qy 592 GAGGTTCCCAACCCAGTCTTCAAGCAAGTGGATGTGATATCTCCTCACTGACGTAAGG 651
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Db 3623 CATTGGAGAGCACGCTG 3642

RESULT 12
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LOCUS BD008404 8418 bp DNA linear PAT 31-JAN-2002
DEFINITION Glyphosate resistant transgenic plants.
ACCESSION BD008404
VERSION BD008404.1 GI:18636777
KEYWORDS JP 2001503280-A/5.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 8418)
AUTHORS Mannerloef, M., Tenning, P. P. and Steen, P.
TITLE Glyphosate resistant transgenic plants
JOURNAL Patent: JP 2001503280-A 5 13-MAR-2001;
NOVARTIS AG
COMMENT OS Unidentified
PN JP 2001503280-A/5
PD 13-MAR-2001
PF 29-OCT-1998 JP 1999525342
PR 31-OCT-1997 US 60/112003
PI MARIE MANNERLOEF, PAUL PETER TENNING, PER STEEN PC
C12N15/82, A01H5/00, A01H5/10
CC Strandedness: Double;
CC Topology: Linear;
FT Key Location/Qualifiers
FT source 1..8418
FT /organism="Unidentified".
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ORIGIN
Query Match 75.3%; Score 554; DB 6; Length 8418;
Best Local Similarity 94.5%; Pred. No. 2.8e-163;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTCGAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
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Qy 176 CAGCTATCTGTCACTTATCAAAAGGACAGTAGAGAAAGAGGTGGCACTTACAAATGCC 235
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Qy 296 ATGACACCCACCACGAGGAGCATCTGTGAAAAAGAGAGGTTCACACACGCTTCAA 355
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Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db 3263 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 3322

Qy 412 AACCTCTCGGATTCATTGCCCCAGCTATCTGTACATTCATCAAAAGGACAGTAGAAAG 471
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Qy 472 GAAGTGGCACTTACAAATGTCATTCATTCGGATAAAGGAAGGCTATCGTTCAAGATGCC 531
Db 3383 GAAGTGGCTCTTACAAATGTCATTCATTCGGATAAAGGAAGGCTATCGTTCAAGATGCC 3442

Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAA 591

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Qy 592 GAGCTTCCCAACCAAGTGGTCCCAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAAGAA 651
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Qy 652 GATGACGACACAATCCCACTATCTCTGCAAGACCCCTCTCTATATAGGAAGTTCATTT 711
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Qy 712 CATTGGAGAGGACACGCTG 731
Db 3623 CATTGGAGAGGACACGCTG 3642

RESULT 13
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LOCUS AR143712 8798 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 4 from patent US 6204436.
ACCESSION AR143712
VERSION AR143712.1 GI:15104998
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 8798)
AUTHORS Mannerloef, M., Tenning, P. Peter. and Steen, P.
TITLE Transgenic plants
JOURNAL Patent: US 6204436-A 4 20-MAR-2001;
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Location/Qualifiers
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ORIGIN
Query Match 75.3%; Score 554; DB 6; Length 8798;
Best Local Similarity 94.5%; Pred. No. 2.8e-163;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTCGAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
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Qy 176 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAGAAAGAGGTGGCACTTACAAATGCC 235
Db 3193 CAGCTATCTGTCACTTTCATCAAAAGGAGTAGTGGAAAGAGGTGGCTCTTACAAATGCC 3252

Qy 236 ATCATTCGGATAAGGAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAG 295
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RESULT 14
BD008403 8798 bp DNA linear PAT 31-JAN-2002
DEFINITION Glyphosate resistant transgenic plants.
ACCESSION BD008403
VERSION BD008403.1 GI:18636776
KEYWORDS JP 2001503280-A/4.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 8798)
AUTHORS Mannerloef,M., Tennig,P.P. and Steen,P.
TITLE Glyphosate resistant transgenic plants
JOURNAL Patent: JP 2001503280-A 4 13-MAR-2001;
NOVARTIS AG
COMMENT OS Unidentified
PN JP 2001503280-A/4
PD 13-MAR-2001
PF 29-OCT-1998 JP 1999525342
PR 31-OCT-1997 US 60/112003
PI MARIE MANNERLOEF,PAUL PETER TENNING,PER STEEN PC
CI:2N15/82,A01H5/00,A01H5/10
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CC Topology: Linear;
FH Key Location/Qualifiers
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Best Local Similarity 94.5%; Pred. No. 2.8e-163;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
Qy 116 TCTCAGTGAGACTTTTCAACAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
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RESULT 15
BD013916
LOCUS Vermin damage-resistant plant.
DEFINITION BD013916
ACCESSION BD013916
VERSION JP 2001112490-A/19.
KEYWORDS unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 661)
AUTHORS Fiskehof,D.A., Fuchs,R.L., Labrik,P.B., Mcpherson,S.A. and
Perlak,F.J.
TITLE Vermin damage-resistant plant
JOURNAL Patent: JP 2001112490-A 19 24-APR-2001;
MONSANTO CO
COMMENT OS Unidentified
PN JP 2001112490-A/19
PD 24-APR-2001
PF 07-SEP-2000 JP 2000272128
PR 29-APR-1987 US 044081
PI DAVID ALLEN FISKEHOF,ROY LEE FUCHS,PAUL BRUNO LABRIK PI
SYLVIA ANNE MCPHERSON,
PI FREDERIC JOSEPH PERLAK
PC CI:2N15/09,A01H5/00,C07K14/325,C12N5/10//C12N1/21,C12P21/02,PC
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Qy 472 GAAGTGGCACTACAAATGCCATCTTGGCATTAAGGAAAGGCTATCGTTCAAGATGCC 531
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 380 GAAGTGGCTCTTACAAATGCCATCTTGGCATTAAGGAAAGGCTATCGTTGAAGATGCC 439
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 532 TCTGCCGACAGTGTCCCAAAGATGGACCCCAACGAGGAGCATCGTGGAAAAGAA 591
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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	734.4	99.8	736	ABS53103	Abs53103 Transgene
2	597.4	81.2	1360	ABS53105	Abs53105 Transgene
3	554	75.3	661	AAN81003	Aan81003 Enhanced
4	554	75.3	661	AAN91710	Aan91710 Enhanced
5	554	75.3	2107	AAD01017	Aad01017 Expressio
6	554	75.3	2122	AAD01015	Aad01015 Expressio
7	554	75.3	2436	AAD01018	Aad01018 Expressio
8	554	75.3	3469	AAD51646	Aad51646 Bacillus
9	554	75.3	3469	10 AAD61794	Aad61794 Bt.cry3Bb
10	554	75.3	3469	10 ABX95190	Abx95190 B. thurin
11	554	75.3	3754	3 AAZ51642	Aaz51642 Bacillus
12	554	75.3	3754	10 AAD61790	Aad61790 Bt.cry3Bb
13	554	75.3	3754	10 ABX95186	Abx95186 B. thurin
14	554	75.3	5170	12 ADK98488	Adk98488 B thuring
15	554	75.3	5600	12 ADK98490	Adk98490 B thuring
16	554	75.3	8012	2 AAX57305	Aax57305 Sugar bee
17	554	75.3	8349	3 AAX15565	Aax15565 PMON30464
18	554	75.3	8418	2 AAX57309	Aax57309 Sugar bee
19	554	75.3	8798	2 AAX57308	Aax57308 Sugar bee
20	551.4	74.9	1030	2 AAV53707	Aav53707 Nucleotid

c	21	551.4	74.9	5796	4	AAH25975	Aah25975 Plant exp
c	22	551.4	74.9	5897	2	AAV63741	Aav63741 Plasmid p
c	23	551.4	74.9	9361	3	AAD01285	Aad01285 Rice tran
c	24	551.4	74.9	10629	3	AAD01286	Aad01286 Rice tran
c	25	550.4	74.8	9335	2	AAV63734	Aav63734 Plasmid p
c	26	550	74.7	10249	3	AAAI5563	Aaai5563 PMON33828
c	27	550	74.7	10312	3	AAAI5564	Aaai5564 PMON33829
c	28	550	74.7	10339	3	AAAI5562	Aaai5562 PMON33827
c	29	549.8	74.7	1030	2	AAQ68893	Aaq68893 Promoter
c	30	548.4	74.5	1030	2	AAQ76263	Aaq76263 PNA lecti
c	31	548.4	74.5	10160	2	AAV63723	Aav63723 Vector pl
c	32	548.4	74.5	11784	2	AAV63724	Aav63724 Vector pl
c	33	548.4	74.5	11991	2	AAV63725	Aav63725 Vector pl
c	34	543.6	73.9	4149	3	AAZ51641	Aaz51641 Bacillus
c	35	543.6	73.9	4149	10	AAD61789	Aad61789 Bt.cry3Bb
c	36	543.6	73.9	4149	10	ABX95185	Abx95185 B. thurin
c	37	534.6	72.6	5767	6	AAI17547	Aai17547 Plasmid p
c	38	534.6	72.6	14446	6	AAI17548	Aai17548 Plasmid p
c	39	526	71.5	829	4	AAF81265	Aaf81265 Cauliflow
c	40	526	71.5	829	9	ADA44822	Ada44822 Cauliflow
c	41	526	71.5	1334	2	AAZ27627	Aaz27627 Plasmid S
c	42	526	71.5	11478	8	ABV75873	Abv75873 Vector pp
c	43	526	71.5	12304	8	ABV75876	Abv75876 Luciferas
c	44	526	71.5	12497	8	ABV75875	Abv75875 Luciferas
c	45	526	71.5	12614	4	AAC66931	Aac66931 Plant sig

ALIGNMENTS

RESULT 1
ABS53103
ID ABS53103 standard; DNA; 736 BP.
XX
AC ABS53103;
XX
DT 29-NOV-2002 (first entry)
XX
DE Transgene expression related bidirectional dual promoter complex #1.
KW Bidirectional dual promoter complex; transcripition; transgene;
KW agronomic performance; transformation; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..736
FT /tag= a
FT /note= "The complement of this sequence is also claimed
in claim 9 as SEQ ID number 2"
XX
PN WO200264804-A2.
XX
PD 22-AUG-2002.
XX
PF 13-FEB-2002; 2002WO-US004188.
XX
PR 13-FEB-2001; 2001US-0268358P.
XX
PA (UYFL) UNIV FLORIDA.
XX
PI Li Z, Gray DJ;
XX
DR WPI; 2002-627601/67.
XX
PT New bi-directional promoter complex comprising a modified enhancer region
including at least 2 enhancer sequences, and at least 2 core promoters,
useful for enhancing or improving transcriptional activity of transgenes.
XX
PS Claim 9; Fig 2; 77pp; English.
XX
CC The invention describes a bi-directional promoter complex comprising a
modified enhancer region that includes at least 2 enhancer sequences, and

CC at least 2 core promoters. The core promoters are on either side of the
CC modified enhancer region in a divergent orientation. The bi-directional
CC promoter complex is useful for enhancing transcriptional activity of
CC transgenes to improve agronomic performance used in genetic
CC transformation with plants. Vectors that include the bi-directional
CC promoter complex may be used to express foreign genes in mammalian cells
CC and in plant cells including dicots and monocots. This sequence
CC represents a bidirectional dual promoter complex useful for enhancing
CC transcriptional activity of transgenes
XX
SQ

Sequence 736 BP; 222 A; 176 C; 175 G; 163 T; 0 U; 0 Other;

Query Match 99.8%; Score 734.4; DB 6; Length 736;

Best Local Similarity 99.9%; Pred. No. 6.9e-232;

Matches 735; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGATCCAGCGTGCCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTCTTTGGC 60
Db 1 GGATCCAGCGTGCCTCTCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTCTTTGGC 60
Qy 61 AAGGATAGTGGATTGTGCGTCACTCCCTTACGTCAGTGGAGATCTGCAGAGCTTCTGC 120
Db 61 AAGGATAGTGGATTGTGCGTCACTCCCTTACGTCAGTGGAGATCTGCAGAGCTTCTGC 120
Qy 121 AGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCTCGGATTCCTCAATGCCCCAGCT 180
Db 121 AGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCTCGGATTCCTCAATGCCCCAGCT 180
Qy 181 ATCTGTCACTTCATCAAAAGGACAGTAGAGAAAGAGGTGGCACCTCAAAATGCCATCAT 240
Db 181 ATCTGTCACTTCATCAAAAGGACAGTAGAGAAAGAGGTGGCACCTCAAAATGCCATCAT 240
Qy 241 TGGATAAAGGAAGGCTATCGTTCAAGATGCGCTCTGCCACAGTGTGTCCTCAAGATGGA 300
Db 241 TGGATAAAGGAAGGCTATCGTTCAAGATGCGCTCTGCCACAGTGTGTCCTCAAGATGGA 300
Qy 301 CCCCCACCCAGGAGCATCGTGGAAAAAGAGACGTTTCCAAACACGCTTCCAAAGCAA 360
Db 301 CCCCCACCCAGGAGCATCGTGGAAAAAGAGACGTTTCCAAACACGCTTCCAAAGCAA 360
Qy 361 GTGGATTGATGTATTCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCTC 420
Db 361 GTGGATTGATGTATTCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCTC 420
Qy 421 GGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAGAAAGAGGTGGC 480
Db 421 GGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAGAAAGAGGTGGC 480
Qy 481 ACCTACAAATGCCATCATTCGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCGGAC 540
Db 481 ACCTACAAATGCCATCATTCGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCGGAC 540
Qy 541 AGTGTCCCAAGATGACCCCAACCCAGAGAGCATCGTGGAAGAAAGAGAGCTTCCA 600
Db 541 AGTGTCCCAAGATGACCCCAACCCAGAGAGCATCGTGGAAGAAAGAGAGCTTCCA 600
Qy 601 ACCAGCTCTTCAAGCAAGTGGATTGATGTATCTCCACTGACGTAAGGGATGAGCA 660
Db 601 ACCAGCTCTTCAAGCAAGTGGATTGATGTATCTCCACTGACGTAAGGGATGAGCA 660
Qy 661 CAATCCCACTATCTTCGCAAGACCTCTCTATATAGGAAGTTCATTTGGAG 720
Db 661 CAATCCCACTATCTTCGCAAGACCTCTCTCTATATAGGAAGTTCATTTGGAG 720
Qy 721 AGACACGCTGGATCC 736
Db 721 AGACACGCTGGATCC 736

RESULT 2

ABS53105

ID ABS53105 standard; DNA; 1360 BP.

XX

AC ABS53105;
XX 29-NOV-2002 (first entry)
XX Transgene expression related bidirectional dual promoter complex #2.
DE Bidirectional dual promoter complex; transgene;
XX agronomic performance; transformation; ds.
KW Synthetic.
XX
XX Key Location/Qualifiers
FT misc_feature 1. .1360
FT /tag= a
FT /note= "The complement of this sequence is also claimed
FT in claim 10 as SEQ ID number 4"
XX
XX WO200264804-A2.
PN 22-AUG-2002.
XX
XX 13-FEB-2002; 2002WO-US004188.
XX 13-FEB-2001; 2001US-0268358P.
PR (UYFL) UNIV FLORIDA.
XX
XX Li Z, Gray DJ;
PI
XX WPI; 2002-627601/67.
XX
XX New bi-directional promoter complex comprising a modified enhancer region
XX including at least 2 enhancer sequences, and at least 2 core promoters,
XX useful for enhancing or improving transcriptional activity of transgenes.
PS Claim 10; Fig 4; 77bp; English.
XX
XX The invention describes a bi-directional promoter complex comprising a
XX modified enhancer region that includes at least 2 enhancer sequences, and
XX at least 2 core promoters. The core promoters are on either side of the
XX modified enhancer region in a divergent orientation. The bi-directional
XX promoter complex is useful for enhancing transcriptional activity of
XX transgenes to improve agronomic performance used in genetic
XX transformation with plants. Vectors that include the bi-directional
XX promoter complex may be used to express foreign genes in mammalian cells
XX and in plant cells including dicots and monocots. This sequence
XX represents a bidirectional dual promoter complex useful for enhancing
XX transcriptional activity of transgenes
SQ Sequence 1360 BP; 353 A; 319 C; 317 G; 371 T; 0 U; 0 Other;
Query Match 81.2%; Score 597.4; DB 6; Length 1360;
Best Local Similarity 99.8%; Pred. No. 1.18e-186;
Matches 598; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 109 AGAAGCTTCTGCAGTGAGACTTTTCAACAAAGGTAATATCGGGAAACCTCTCGGATTC 168
Db 762 ATGAAGCTTCTGCAGTGAGACTTTTCAACAAAGGTAATATCGGGAAACCTCTCGGATTC 821
Qy 169 CATTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAGAAAGAGGTGGACCTAC 228
Db 822 CATTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAGAAAGAGGTGGACCTAC 881
Qy 229 AATGCGCATCTTCGATTAAGGAGGCTATCGTTCAAGATGCCCTCTGCCGACAGTGGT 288
Db 882 AATGCGCATCTTCGATTAAGGAGGCTATCGTTCAAGATGCCCTCTGCCGACAGTGGT 941
Qy 289 CCAAGAGATGGACCCCAACCCAGAGAGCATCGTGGAAGAAAGAGAGCTTCCAACACAG 348
Db 942 CCAAGAGATGGACCCCAACCCAGAGAGCATCGTGGAAGAAAGAGAGCTTCCAACACAG 1001
Qy 349 TCTTCAAGCAAGTGGATGTGATTTGCAGTGAGACTTTTCAACAAAGGTAATATCG 408
XX

Db 1002 TCTTCAAGCAAGTGGATTGATGATGCGAGTCTTTCACAAAGGTTAATATCG 1061
 Qy 409 GGAACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAA 468
 Db 1062 GGAACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAA 1121.
 Qy 469 AAGGAAGTGGCAGCTACAAATGCATTCATTCGATTAAGAAAGGCTATCGTTCAAGAT 528
 Db 1122 AAGGAAGTGGCAGCTACAAATGCATTCATTCGATTAAGAAAGGCTATCGTTCAAGAT 1181
 Qy 529 GCCTCTGCGGACAGTGGTCCAAAGATGGACCCACCACGAGGAGCATCGTGGAAAAA 588
 Db 1182 GCCTCTGCGGACAGTGGTCCAAAGATGGACCCACCACGAGGAGCATCGTGGAAAAA 1241
 Qy 589 GAAGACGTTCCAAACCAAGTCTTCAAGCAAGTGGATGATGATGATATCTCCACTGACGTA 648
 Db 1242 GAAGACGTTCCAAACCAAGTCTTCAAGCAAGTGGATGATGATGATATCTCCACTGACGTA 1301
 Qy 649 AGGATGACGACAAATCCCACTATCTTCCGCAAGCCCTTCTCTATATAGGAAGTTC 707
 Db 1302 AGGATGACGACAAATCCCACTATCTTCCGCAAGCCCTTCTCTATATAGGAAGTTC 1360

RESULT 3

AAN81003
 ID AAN81003 standard; DNA; 661 BP.
 AC
 AC AAN81003;

XX 03-NOV-1990 (first entry)

DE Enhanced CamV35S promoter used in pMON893 *B. thuringiensis* toxin prodn.

XX *Bacillus thuringiensis* var. *tenebrionis* toxin gene; enhanced promoter;
 KW CamV35S; pMON893; Coleopteran insects; transformed plants;
 KW chimaeric gene; ss.

XX *Bacillus thuringiensis*.

XX Key Location/Qualifiers

FT misc_feature 27..279

FT /*tag= a

FT /number= 1

FT /note= "duplicated enhancer"

FT 289..541

FT /*tag= b

FT /number= 2

FT /note= "duplicated enhancer"

XX EP289479-A.

XX 02-NOV-1988.

XX 26-APR-1988; 88EP-00870070.

XX 29-APR-1987; 87US-00044081.

XX (MONS) MONSANTO CO.

XX Fischhoff DA, Fuchs RL, Mcpherson SA, Lavrik PB, Perlak FJ;

XX WPI; 1988-309416/44.

XX Genetically transformed plants with toxicity to Coleopteran insects -

XX obtd. using chimeric gene contg. sequence encoding toxin protein of

XX *Bacillus thuringiensis*.

XX Disclosure; Page ?; 52pp; English.

XX A fragment of the CamV35S promoter (-343 to +9), previously constructed

XX by Odell et al. (1985) Nature 313:810-812, is necessary for maximal

XX expression of the promoter. It was excised as a *Clar*-*HindIII* fragment,

XX made blunt ended with DNA pol I and inserted into the *HindIII* site of

CC pUC18. The upstream region of the 35S promoter was excised from this
 CC plasmid as a *HindIII*-*EcoRV* fragment (-343 to -90) and inserted into the
 CC same plasmid between the *HindIII* and *PstI* sites. The enhanced promoter
 CC thus contains a duplication of sequences -343 to -90. See also AAN81000-
 CC N81003

SQ Sequence 661 BP; 194 A; 160 C; 157 G; 150 T; 0 U; 0 Other;

Query Match 75.3%; Score 554; DB 1; Length 661;

Best Local Similarity 94.5%; Pred. No. 2.9e-172;

Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTGCGTGTGAGCTTTTCAACAAAGGTTAATATCGGAAACCTCTCGGATTCATTGCC 175
 Db 20 TCCGATGTGAGACTTTTCAACAAAGGTTAATATCGGAAACCTCTCGGATTCATTGCC 79

Qy 176 CAGCTATCTGCTCACTTCATCAAAAGGACAGTAGAAAAGGAGGTGGCACCTACAAATGCC 235

Db 80 CAGCTATCTGCTCACTTTTGTGAAGATAGTGGAAAAGGAGGTGGCTCTTACAAATGCC 139

Qy 236 ATCATTTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGTGGTCCCAAAG 295

Db 140 ATCATTTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGTGGTCCCAAAG 199

Qy 296 ATGGAACCCCAACCCACGAGGAGCATCGTGGAAAAGGAGGTGGCACCTACAAATGCC 355

Db 200 ATGGAACCCCAACCCACGAGGAGCATCGTGGAAAAGGAGGTGGCACCTACAAATGCC 259

Qy 356 AGCAAGTGGATTGATGTGAT ---TGCAGTGAGACTTTTCAACAAAGGTTAATATCGGA 411

Db 260 AGCAAGTGGATTGATGTGATGTGTCGCGATGTGAGACTTTTCAACAAAGGTTAATATCGGA 319

Qy 412 AACTCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 471

Db 320 AACTCTCTCGGATTCATTCGCCAGCTATCTGTCACTTTATGTGAAGATAGTGGAAAAG 379

Qy 472 GAAGTGGGACCTACAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC 531

Db 380 GAAGTGGGCTCTACAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTTGAAGATGCC 439

Qy 532 TCTGCCGACAGTGTGCCAAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAGAA 591

Db 440 TCTGCCGACAGTGTGCCAAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAGAA 499

Qy 592 GAGCTTCCAAACCCAGCTTTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG 651

Db 500 GAGCTTCCAAACCCAGCTTTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG 559

Qy 652 GATGAGGACAAATCCCACTATCTTCCGAAAGCCCTTCTCTATATAGGAAGTTCATT 711

Db 560 GATGAGGACAAATCCCACTATCTTCCGAAAGCCCTTCTCTATATAGGAAGTTCATT 619

Qy 712 CATTTGGAGAGGACACGCTG 731

Db 620 CATTTGGAGAGGACACGCTG 639

RESULT 4

AAN91710

ID AAN91710 standard; DNA; 661 BP.

XX AAN91710;

XX 25-MAR-2003 (revised)

DT 12-MAR-1990 (first entry)

XX Enhanced CamV35S promoter used in plasmid pMON893.

XX CamV35S promoter; *Bacillus thuringiensis*; toxin protein; insecticide;

XX plasmid pMON893.

XX Cauliflower mosaic virus.

XX

CC herbicides such as glyphosate and AMPA tolerance, in recombinant plants
CC and to prevent self-fertilisation and enhance hetero-fertilisation. The
CC present DNA sequence is the expression cassette-2, comprising a plant
CC operable promoter and 5' sequences like, 5' untranslated region (UTR) and
CC intron, linked to modified E. coli phnO coding region encoding P2A AMPA
CC acyltransferase (AAT) enzyme and plant operable termination sequences
XX
SQ Sequence 2122 BP; 495 A; 537 C; 561 G; 529 T; 0 U; 0 Other;

Query Match 75.3%; Score 554; DB 3; Length 2122;
Best Local Similarity 94.5%; Pred. No. 5.1e-172;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTCGAGTGAGACTTTTCAACAAGGGTAAATATCGGAAACCTCTCGGATTCATTGCC 175
Db 8 TCCGATGTGAGACTTTTCAACAAGGGTAAATATCGGAAACCTCTCGGATTCATTGCC 67

Qy 176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAGAAAGAGGTGGCCCTACAAATGCC 235
Db 68 CAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAGAGGTGGCTCTACAAATGCC 127

Qy 236 ATCATTCGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCAAAG 295
Db 128 ATCATTCGGATAAAGGAAAGGCCATCGTTGAAGATGCTCTGCCGACAGTGGTCCAAAG 187

Qy 296 ATGGACCCCCACCCACGAGGAGCATCGTTGGAAGAAAGAGCGTTTCCACACCGTCTTCAA 355
Db 188 ATGGACCCCCACCCACGAGGAGCATCGTTGGAAGAAAGAGCGTTTCCACACCGTCTTCAA 247

Qy 356 AGCAAGTGGATTGATGTGAT-----TGCACTGAGACTTTTCAACAAAGGGTAATATCGGA 411
Db 248 AGCAAGTGGATTGATGTGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCG 307

Qy 412 AACCTCTCGGATTCGATTCGCGAGCTATCTGTCACTTCATCAAAAGGACAGTAGAGAAAG 471
Db 308 AACCTCTCGGATTCGATTCGCGAGCTATCTGTCACTTCATCAAAAGGACAGTAGAGAAAG 367

Qy 472 GAAGTGGCAGCTACAAATGCCATCATTTGCGATAAGAGGAGGCTATCGTTCAAGATGCC 531
Db 368 GAAGTGGCTCTCAAAATGCCATCATTTGCGATAAGAGGAGGCTATCGTTCAAGATGCC 427

Qy 532 TCTGCCGACAGTGTGCCAAAGATGGACCCGCCACGAGGAGCATCGTGGAAAAAGAA 591
Db 428 TCTGCCGACAGTGTGCCAAAGATGGACCCGCCACGAGGAGCATCGTGGAAAAAGAA 487

Qy 592 GACGTTCCACACCGCTCTCAAGCAAGTGATGATGATGATGATGATGATGATGATGATGATG 651
Db 488 GACGTTCCACACCGCTCTCAAGCAAGTGATGATGATGATGATGATGATGATGATGATGATG 547

Qy 652 GATGACGACAAATCCCACTATCTTCGCAAGACCTTCTCTATATAAGGAAGTTCATTT 711
Db 548 GATGACGACAAATCCCACTATCTTCGCAAGACCTTCTCTATATAAGGAAGTTCATTT 607

Qy 712 CATTTGGAGAGGACACGCTG 731
Db 608 CATTTGGAGAGGACACGCTG 627

RESULT 7
AAD01018
ID AAD01018 standard; DNA; 2436 BP.

XX AC AAD01018;
XX
XX 21-SEP-2000 (first entry)
XX DE Expression cassette-5 comprising modified E. coli P2A phnO coding gene.
XX
XX Phosphonate herbicide tolerance; aminomethyl phosphonic acid; AMPA; AAT;
KW acyltransferase; transacylase; recombinant plant; expression cassette;
KW corn; tobacco; wheat; cotton; canola; rice; chloroplast transit peptide;
KW CTP; glyophosate oxidase; GOX; glyophosate oxidoreductase; phnO gene;
KW self-fertilisation; hetero-fertilisation; ds.

XX Escherichia coli.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT promoter 26..640
FT /tag= a
FT /note= "plant functional heterologous promoter"
FT intron 670..1473
FT /tag= b
FT /note= "Enhances expression of the phnO gene"
FT transit_peptide 1498..1725
FT /tag= c
FT /note= "Targets the protein to an intracellular
FT organelle, like chloroplast"
FT 1726..2160
FT /tag= d
FT /product= "Escherichia coli modified P2A AMPA
FT acyltransferase (AAT) enzyme"
FT /function= "Transfers acyl group from an acylcarrier
FT (CoA) to the free amino group of aminomethylphosphonate"
FT terminator 2172..2427
FT /tag= e
XX WO2000029596-A1.
PN
XX 25-MAY-2000.
PD
XX
XX 16-NOV-1999; 99WO-US027152.
PF
XX 17-NOV-1998; 98US-0108763P.
PR
XX (MONS) MONSANTO CO.
PA
XX Barry GF;
PI
XX WPI; 2000-387806/33.
DR P-PSDB; AAY71251.
XX
XX Enhancing phosphonate herbicide tolerance in corn, tobacco, wheat,
PT cotton, canola and rice plants involves transforming plants with
PT phosphonate metabolizing genes encoding acyltransferase enzyme.
XX
XX Disclosure; Page 173-175; 179pp; English.
XX
XX The patent discloses a method for selectively enhancing the phosphonate
CC herbicide tolerance in recombinant corn, tobacco, wheat, cotton, canola
CC and rice plants, by transforming the plants with an expression cassette.
CC It comprises of a structural DNA sequence, that encodes an aminomethyl
CC phosphonic acid (AMPA) acyltransferase or transacylase (AAT), capable of
CC N-acylation of AMPA. This sequence has an amino terminal chloroplast
CC transit peptide (CTP), that targets AAT to the chloroplast. Co-expression
CC of glyphosate oxidase (GOX) gene, encoding glyphosate oxidoreductase,
CC along with AAT provides the transformed plants with higher resistance to
CC phosphonate herbicides. This method is useful for enhancing phosphonate
CC herbicides such as glyphosate and AMPA tolerance, in recombinant plants
CC and to prevent self-fertilisation and enhance hetero-fertilisation. The
CC present DNA sequence is the expression cassette-5, comprising a plant
CC operable promoter and 5' sequences like intron, linked to modified E.
CC coli phnO coding region, encoding P2A AMPA acyltransferase (AAT) enzyme
CC and plant operable termination sequences
XX
SQ Sequence 2436 BP; 634 A; 565 C; 567 G; 670 T; 0 U; 0 Other;

Query Match 75.3%; Score 554; DB 3; Length 2436;
Best Local Similarity 94.5%; Pred. No. 5.5e-172;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTCGAGTGAGACTTTTCAACAAGGGTAAATATCGGAAACCTCTCGGATTCATTGCC 175
Db 28 TCCGATGTGAGACTTTTCAACAAGGGTAAATATCGGAAACCTCTCGGATTCATTGCC 87

Qy 176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAGAAAGGAGGTGGCCACCTACAAATGCC 235

```

Db 88 CAGCTATCTGTCACCTTTATTTGTAAGATAGTGGAAAGGAAAGGTTGGCTCTCTACAAATGCC 147
Qy 236 ATCATTTGGATAAAGAAAGGCTATCGTTTCAAGATGCTCTGCGCACAGTAGTGGTCCCAAAG 295
Db 148 ATCATTTGGATAAAGAAAGGCTATCGTTTGAAGATGCTCTGCGCACAGTAGTGGTCCCAAAG 207
Qy 296 ATGGACCCCAACCAACGAGGAGCATCGTTGGAAAAAGAAAGAGAGTTCCCAACCAAGCTTTCAA 355
Db 208 ATGGACCCCAACCAACGAGGAGCATCGTTGGAAAAAGAAAGAGAGTTCCCAACCAAGCTTTCAA 267
Qy 356 AGCAAGTGGATTGATGTCAT---TGCAGTGCAGACTTTTCAACAAAGGTAATATCCGGA 411
Db 268 AGCAAGTGGATTGATGTCATGTCGATGTCGATGTCGAGACTTTTCAACAAAGGTAATATCCGGA 327
Qy 412 AACCTCTCTCGGATTCATTTGGCCAGCTATCTGTCTACATTTTCATCAAAAGGACAGTAGAGAAAG 471
Db 328 AACCTCTCTCGGATTCATTTGGCCAGCTATCTGTCTACATTTTCATCAAAAGGACAGTAGAGAAAG 387
Qy 472 GAAGTGGACACTCAAAATGCCATCATTTGGCGATTAAGAAAGGCTATCGTTCAAGATGCC 531
Db 388 GAAGTGGCTCTCTACAAATGCCATCATTTGGCGATTAAGAAAGGCTATCGTTCAAGATGCC 447
Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCAGGAGCATCGTGGAAAGAA 591
Db 448 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCAGGAGCATCGTGGAAAGAA 507
Qy 592 GACGTTCCCAACCAAGCTCTTCAAGCAAGTGAATGATGATATCTCCACTGACGTAAGG 651
Db 508 GACGTTCCCAACCAAGCTCTTCAAGCAAGTGAATGATGATATCTCCACTGACGTAAGG 567
Qy 652 GATGAGCACAATCCCACTATCTCTTCCAAAGCCCTTCTCTATATAAGGAAGTTCAATTT 711
Db 568 GATGAGCACAATCCCACTATCTCTTCCAAAGCCCTTCTCTATATAAGGAAGTTCAATTT 627
Qy 712 CATTGGAGGACACGCTG 731
Db 628 CATTGGAGGACACGCTG 647

RESULT 8
AAZ51646
ID AAZ51646 standard; DNA; 3469 BP.
XX AC AAZ51646;
XX AC
XX AC
DT 15-SEP-2003 (revised)
DT 21-JUN-2000 (first entry)
XX

DE Bacillus thuringiensis Cry3Bb variant 11231mv2 expression cassette-2.
XX
XX delta-endotoxin; Cry3B; Bt toxin; crystal protein; insect pest;
KW insecticide; Coleopteran; expression cassette; transgenic plant;
KW Cry3Bb variant 11231mv2; ds.
XX
XX Cauliflower mosaic virus.
OS Triticum aestivum.
OS Oryza sativa.
OS Bacillus thuringiensis.
OS Chimeric.
XX

Key Location/Qualifiers
FH promoter 25..640
FT /*tag= a
FT /*label= P-CaWV.35S
FT 5'UTR 664..734
FT /*tag= b
FT /*label= L-Ta.hcb1
FT /*note= "Wheat chlorophyll A/B binding protein
FT untranslated leader sequence"
FT 748..1238
FT /*tag= c
FT /*label= I-Os.Act1
FT
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```

FT CDS
FT /note= "Rice actin intron sequence"
FT 1241..3202
FT /*tag= d
FT /product= "Cry3Bb variant 11231mv2"
FT terminator 3217..3450
FT /*tag= e
FT /label= "T-Ta.hspl7
FT /note= "Wheat heat shock Hspl7 transcription termination
FT and polyadenylation sequence"
XX
XX WO200011185-A2.
XX
XX 02-MAR-2000.
XX
XX 19-AUG-1999; 99WO-US018883.
XX
XX 19-AUG-1998; 98US-0097150P.
XX (MONS ) MONSANTO CO.
XX
XX Romano CP;
XX
XX WPI: 2000-246568/21.
XX P-PSDB; AAY70446.
XX
XX Novel expression cassettes which express Bacillus thuringiensis Cry3
XX delta-endotoxin portion which is toxic to coleopteran insect pests,
XX useful for producing transgenic plants with improved insecticidal
XX activity.
XX
XX Claim 16; Page 149-152; 171pp; English.
XX
XX The present sequence is an expression cassette from a Cry3Bb plant
XX expression vector pMON33748. It comprises an enhanced Cauliflower mosaic
XX virus (CaWV) 35S promoter sequence, a wheat chlorophyll A/B binding
XX protein untranslated leader sequence, a rice actin intron sequence, a
XX Bacillus thuringiensis delta-endotoxin Cry3Bb variant 11231mv2 coding
XX sequence and a wheat heat shock Hspl7 transcription termination and
XX polyadenylation sequence. This expression cassette is used to improve
XX expression of Cry3B variant protein in transgenic plants e.g. maize, to
XX increase insecticidal activity against Coleopteran pests. (Updated on 15-
XX SEP-2003 to standardise OS field)
XX
SQ Sequence 3469 BP; 790 A; 1078 C; 845 G; 756 T; 0 U; 0 Other;
Query Match 75.3%; Score 554; DB 3; Length 3469;
Best Local Similarity 94.5%; Pred. No. 6.5e-172;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
```

```

Qy 116 TCTGCAGTGAGACTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCATTTGCC 175
Db 28 TCCGATGTGAGACTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCATTTGCC 87
Qy 176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAGGTGGCACCTACAAATGCC 235
Db 88 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAGGTGGCTCTCAAAATGCC 147
Qy 236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTCGGACAGTGGTCCCAAAG 295
Db 148 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTCGGACAGTGGTCCCAAAG 207
Qy 296 ATGGACCCCAACCCAGGAGGAGCATCGTTGAAAAAGAAAGAGCTTTCAACCAAGCTTTCAA 355
Db 208 ATGGACCCCAACCCAGGAGGAGCATCGTTGAAAAAGAAAGAGCTTTCAACCAAGCTTTCAA 267
Qy 356 AGCAAGTGGATTGATGTCAT---TGCAGTGCAGACTTTTCAACAAAGGTAATATCCGGA 411
Db 268 AGCAAGTGGATTGATGTCATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCG 327
Qy 412 AACCTCTCTCGGATTCATTTGGCCAGCTATCTGTCTACATTTTCATCAAAAGGACAGTAGAAAG 471
Db 328 AACCTCTCTCGGATTCATTTGGCCAGCTATCTGTCTACATTTTCATCAAAAGGACAGTAGAAAG 387
```

Qy	472	GAAGGTGGCCACCTACAAATGCCATTCATTGGGATAAAGGAAAGGCTATCGTTCAAGATGCC	531	XX	New transgenic plant resistant to Coleopteran pests, comprises <i>Bacillus thuringiensis</i> Cry3-delta-endotoxin gene.
Db	388	GAAGTGGCTCCTACAAATGCCATTCATTGGGATAAAGGAAAGGCTATCGTTGAAGATGCC	447	PT	
Qy	532	TCGCGCGACAGTGGTCCAAAGATGGACCCGCCACCCACGAGGAGCATCGTGGAAAAAGAA	591	PS	Claim 16; Page 77-80; Opp; English.
Db	448	TCGCGCGACAGTGGTCCAAAGATGGACCCGCCACCCACGAGGAGCATCGTGGAAAAAGAA	507	XX	The invention relates to novel transgenic plants comprising <i>Bacillus thuringiensis</i> Cry3-delta-endotoxin gene or its variants having
Qy	592	GAGTTCACCAACCGCTCTTCAAGCAAGTGGATTGATGTCATATCTCCACTGACGTAAGG	651	CC	Coleopteran inhibitory activity. The invention is useful for controlling
Db	508	GAGTTCACCAACCGCTCTTCAAGCAAGTGGATTGATGTCATATCTCCACTGACGTAAGG	567	CC	Coleopteran insect infestation in a field of crop plants. The present
Qy	652	GATGACGCACAATCCCACTATCTCTTCGCAAGACCTTCCTCTATATAAGGAAGTTCATTT	711	CC	sequence is <i>B. thuringiensis</i> Cry3Bb-delta- endotoxin variant expression
Db	568	GATGACGCACAATCCCACTATCTCTTCGCAAGACCTTCCTCTATATAAGGAAGTTCATTT	627	XX	vector DNA
Qy	712	CATTGGAGGACACGCTG 731		Qy	Sequence 3469 BP; 790 A; 1078 C; 845 G; 756 T; 0 U; 0 Other;
Db	628	CATTGGAGGACACGCTG 647		XX	
RESULT 9					
AAD61794					Query Match 75.3%; Score 554; DB 10; Length 3469;
XX	AAD61794				Best Local Similarity 94.5%; Pred. No. 6.5e-172;
AC	AAD61794;				Matches 586; Conservative 0; Mismatches 4; Gaps 1;
XX					
DT	15-JAN-2004	(first entry)			
XX	Bt.cry3Bb.11231mv2	expression vector DNA, pMON33748.			
DE					
XX					
KW	Transgenic plant; Cry3Bb-delta-endotoxin; Coleopteran pest resistance;				
KW	insecticide; variant; cyclic; circular; chimeric; rice; wheat; gene; ds.				
XX					
OS	Chimeric - Cauliflower mosaic virus.				
OS	Chimeric - Oryza sativa.				
OS	Chimeric - <i>Bacillus thuringiensis</i> .				
OS	Chimeric - <i>Triticum aestivum</i> .				
XX					
PH	Key	Location/Qualifiers			
FT	promoter	25..640			
FT		/*tag= a			
FT		/note= "Cauliflower mosaic virus 35S promoter (P-			
FT		CaMV.35S)"			
FT	misc_feature	664..734			
FT		/*tag= b			
FT		/note= "Wheat chlorophyll A/B binding protein			
FT		untranslated leader sequence (L-Ta.hcbl)"			
FT	intron	748..1238			
FT		/*tag= c			
FT		/note= "Rice actin intron (I-Os.Act1)"			
FT	CDS	1241..3202			
FT		/*tag= d			
FT		/product= "Bt.cry3Bb.11231mv2 protein"			
FT	misc_feature	3217..3420			
FT		/*tag= e			
FT		/note= "Wheat heat shock Hsp117 transcription termination			
FT		and polyadenylation sequence (T-Ta.Hsp117)"			
XX					
PN	US2003115630-A1.				
XX					
PD	19-JUN-2003.				
XX					
PF	29-AUG-2002; 2002US-00232665.				
XX					
PR	19-AUG-1999; 99US-00377466.				
XX					
PA	(ROMA/) ROMANO C P.				
XX					
PI	Romano CP;				
XX					
DR	WPI; 2003-810928/76.				
DR	P-PSDB; ABW01055.				
DR					

XX Cry3Bb1 11231mv2; gene; delta-endotoxin; plant; transgenic; insecticide; insecticide;
 KW crystal 3; Cry3; Coleopteran insect infestation; increased toxicity; ds;
 KW season long protection; beetle; maize; rice; expression cassette.
 XX Bacillus thuringiensis.
 OS Zea mays.
 OS Oryza sativa.
 OS Cauliflower mosaic virus.
 OS Synthetic.
 XX Key Location/Qualifiers
 PH 25..640
 FT promoter
 FT /*tag= a
 FT /note= "Enhanced CMV35S promoter"
 FT 664..734
 FT 5'UTR
 FT /*tag= b
 FT /note= "Wheat chlorophyll A/B binding protein
 FT untranslated leader sequence"
 FT 748..1238
 FT intron
 FT /*tag= c
 FT /number= 1
 FT /cons splice= (5'site:NO,3'site:NO)
 FT /note= "Rice actin intron"
 FT 1241..3202
 FT CDS
 FT /*tag= d
 FT /product= "Cry3Bb1 11231mv2"
 FT 3217..3450
 FT misc_signal
 FT /*tag= e
 FT /note= "Wheat heat shock HSP17 transcription terminator
 FT and polyadenylation sequence"
 FT US6501009-B1.
 XX 31-DEC-2002.
 XX 19-AUG-1999; 99US-00377466.
 XX 19-AUG-1999; 99US-00377466.
 XX (MONS) MONSANTO TECHNOLOGY LLC.
 XX Romano CP;
 XX WPI; 2003-352192/33.
 XX P-PSDB; ABU09202.
 XX New modified polynucleotide useful for controlling Coleopteran insect
 FT infestation in a field of crop plants encodes insecticidal crystal 3
 XX Bacillus thuringiensis delta-endotoxin.
 XX Disclosure; Col 141-148; 107pp; English.
 XX The invention relates to a modified polynucleotide which encodes an
 CC insecticidal crystal 3 (Cry3) Bacillus thuringiensis delta-endotoxin such
 CC as Cry3Bb. The modified polynucleotide is useful for producing a
 CC transformed cell, by introducing the modified polynucleotide into a cell
 CC such as a plant cell (preferably a maize cell) or a microbial cell. The
 CC modified polynucleotide is useful for producing a transformed maize plant
 CC by introducing the modified polynucleotide into a maize plant cell,
 CC selecting a transformed maize plant cell and regenerating a maize plant
 CC from the transformed maize plant cell. A transgenic plant expressing the
 CC modified polynucleotide is useful for controlling Coleopteran insect
 CC infestation in a field of crop plants. The modified polynucleotide is
 CC useful for producing transgenic plants expressing higher levels of the
 CC insect controlling B. thuringiensis delta-endotoxin. The modified
 CC polynucleotide provides up to 10 fold higher levels of insect controlling
 CC delta-endotoxin relative to the highest levels obtained using prior
 CC compositions. In particular, transgenic maize expressing higher levels of
 CC the Cry3Bb protein designed to exhibit increased toxicity toward
 CC Coleopteran pests deliver superior levels of insect protection and are
 CC less likely to sponsor development of populations of target insects that
 CC are resistant to the insecticidally active protein. Improved control of

CC susceptible target insect pests and season long protection from insect
 CC pathogens is achieved using the modified polynucleotide. The modified
 CC polynucleotide reduces the number of transgenic events that have to be
 CC screened in order to identify one which contains beneficial levels of one
 CC or more insect controlling compositions. The present sequence represents
 CC Bacillus thuringiensis delta endotoxin Cry3Bb1 11231mv2 expression
 CC cassette #2 DNA
 XX
 SQ Sequence 3469 BP; 790 A; 1078 C; 845 G; 756 T; 0 U; 0 Other;
 Query Match 75.3%; Score 554; DB 10; Length 3469;
 Best Local Similarity 94.5%; Pred. No. 6 5e-172;
 Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
 Qy 116 TCTCGAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
 Db |||
 Qy 28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 87
 Db |||
 Qy 176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAGGTGGCACCCTACAAATGCC 235
 Db |||
 Qy 88 CAGCTATCTGTCACTTTTATTGTGAAGATAGTGGAAAAGGAGGTGGCTCTCAAAATGCC 147
 Db |||
 Qy 236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAG 295
 Db |||
 Qy 148 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAG 207
 Db |||
 Qy 296 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAGGAGGTGGTCCCAACACGCTTTCAA 355
 Db |||
 Qy 208 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAGGAGGTGGTCCCAACACGCTTTCAA 267
 Db |||
 Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACATTTTCAACAAAGGTTAATATCGGA 411
 Db |||
 Qy 268 AGCAAGTGGATTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTG 327
 Db |||
 Qy 412 AACCTCTCGGATTTCCATTGCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAG 471
 Db |||
 Qy 328 AACCTCTCGGATTTCCATTGCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAG 387
 Db |||
 Qy 472 GAAGGTGGACCTACAAATGCCATTCATTCGATAAAGGAGGTGGTTCGATGAGATGCC 531
 Db |||
 Qy 388 GAAGGTGGCTCTACAAATGCCATTCATTCGATAAAGGAGGTGGTTCGATGAGATGCC 447
 Db |||
 Qy 532 TCTGCCGACAGTGTGCCAAAGATGGACCCCCACGAGGAGCATCGTGGAAAAGGAA 591
 Db |||
 Qy 448 TCTGCCGACAGTGTGCCAAAGATGGACCCCCACGAGGAGCATCGTGGAAAAGGAA 507
 Db |||
 Qy 592 GAGCTTCCAAACCCAGCTCTTCAAAAGCAGTGTGATGTGATATCTCCACTGACGTAAAG 651
 Db |||
 Qy 508 GAGCTTCCAAACCCAGCTCTTCAAAAGCAGTGTGATGTGATATCTCCACTGACGTAAAG 567
 Db |||
 Qy 652 GATGACGCACAATCCCACTATCTTTCGAAAGACCTTCTCTATATAGGAGTTCATTT 711
 Db |||
 Qy 568 GATGACGCACAATCCCACTATCTTTCGAAAGACCTTCTCTATATAGGAGTTCATTT 627
 Db |||
 Qy 712 CATTGGAGAGGACACGCTG 731
 Db |||
 Qy 628 CATTGGAGAGGACACGCTG 647
 Db |||
 RESULT 11
 AAZ51642
 ID AAZ51642 standard; DNA; 3754 BP.
 XX AC
 XX AAZ51642;
 XX AC
 XX 15-SEP-2003 (revised)
 DT 21-JUN-2000 (first entry)
 XX DE
 XX Bacillus thuringiensis Cry3Bb variant v11231 expression cassette-2.
 KW delta-endotoxin; Cry3B; Bt toxin; crystal protein; insect pest;
 KW insecticide; Coleopteran; expression cassette; transgenic plant;
 KW Cry3Bb variant v11231; ds.


```
PF 29-AUG-2002; 2002US-002322665.
XX
XX 19-AUG-1999; 99US-00377466.
XX (ROMA/) ROMANO C P.
XX Romano CP;
XX
XX WPI; 2003-810928/76.
XX P-PSDB; ABW01053.
XX
XX New transgenic plant resistant to Coleopteran pests, comprises Bacillus
XX thuringiensis Cry3-delta-endotoxin gene.
XX
XX Claim 16; Page 57-60; Opp; English.
XX
XX The invention relates to novel transgenic plants comprising Bacillus
XX thuringiensis Cry3-delta-endotoxin gene or its variants having
XX coleopteran inhibitory activity. The invention is useful for controlling
XX coleopteran insect infestation in a field of crop plants. The present
XX sequence is B. thuringiensis Cry3Bb-delta- endotoxin variant expression
XX vector DNA
XX
XX SQ Sequence 3754 BP; 1030 A; 889 C; 800 G; 1035 T; 0 U; 0 Other;
XX
XX Query Match 75.3%; Score 554; DB 10; Length 3754;
XX Best Local Similarity 94.5%; Pred. No. 6.7e-172;
XX Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
XX
XX 116 TCTGAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 87
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 176 CAGTATCTGCTCATTCAATCAAAAGGACAGTAGAGAGAGGAGGACCTACAAATGCC 235
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 88 CAGTATCTGCTCATTCAATCAAAAGGAGTAGAGAGAGGAGGAGGAGGAGGAGGAGG 147
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 236 ATCAATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTCGGACACAGTGGTCCCAAG 295
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 148 ATCAATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTCGGACACAGTGGTCCCAAG 207
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 296 ATGACACCCACCCACGAGGAGCATCTGTTGAAAAAGAGAGCTTCCAAACAGCTTCAA 355
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 208 ATGACACCCACCCACGAGGAGCATCTGTTGAAAAAGAGAGCTTCCAAACAGCTTCAA 267
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 356 AGCAAGTGATGATGCTAT---TGCAAGTGAGACTTTTCAACAAAGGTAATATCGGA 411
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 268 AGCAAGTGATGATGATGCTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 327
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 412 AACCTCTCGGATTCATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 471
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 328 AACCTCTCGGATTCATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 387
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 472 GAAGTGCGACCTACAAATGCGATTCATTGCGATAAAGGAGGAGGAGGAGGAGGAGGAG 531
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 388 GAAGTGCGCTCTACAAATGCGATTCATTGCGATAAAGGAGGAGGAGGAGGAGGAGGAG 447
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 532 TCTGCGGAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 591
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 448 TCTGCGGAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 507
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 592 GACGTTTCAACACCATCTTCAAGCAAGTGATGATGATGATGATGATGATGATGATGATG 651
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 508 GACGTTTCAACACCATCTTCAAGCAAGTGATGATGATGATGATGATGATGATGATGATG 567
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 652 GATGACGCAATATCCATATCTTTCGCAAGACCCCTTCTCTATATATAGGAAGTTCAATT 711
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 568 GATGACGCAATATCCATATCTTTCGCAAGACCCCTTCTCTATATATAGGAAGTTCAATT 627
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 712 CATTTGGAGAGACAGCTG 731
XX | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 628 CATTTGGAGAGACAGCTG 647
```

```
RESULT 13
ABX95186
ID ABX95186 standard; DNA; 3754 BP.
XX
XX AC ABX95186;
XX
XX 12-JUN-2003 (first entry)
XX
XX B. thuringiensis delta endotoxin Cry3Bb1v1231 expression cassette #2.
XX
XX Cry3Bb1v1231; ds; gene; delta-endotoxin; plant; transgenic; insecticide;
XX crystal 3; Cry3; Coleopteran insect infestation; increased toxicity;
XX season long protection; beetle; maize; expression cassette.
XX
XX Bacillus thuringiensis.
XX
XX Zea mays.
XX Agrobacterium tumefaciens.
XX Cauliflower mosaic virus.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX promoter 25..640
XX /tag= a
XX /note= "Enhanced CaMV35S promoter"
XX intron 669..1472
XX /tag= b
XX /number= 1
XX /cons_splice= (5'site:NO,3'site:NO)
XX /note= "Zea mays HSP70 intron"
XX CDS 1490..3451
XX /tag= c
XX /product= "Cry3Bb1v1231"
XX misc_signal 3475..3730
XX /tag= d
XX /note= "Agrobacterium tumefaciens nopaline synthase"
XX transcription terminator and polyadenylation sequence"
XX
XX US6501009-B1.
XX
XX 31-DEC-2002.
XX
XX 19-AUG-1999; 99US-00377466.
XX
XX 19-AUG-1999; 99US-00377466.
XX (MONS ) MONSANTO TECHNOLOGY LLC.
XX Romano CP;
XX
XX WPI; 2003-352192/33.
XX P-PSDB; ABU09198.
XX
XX New modified polynucleotide useful for controlling Coleopteran insect
XX infestation in a field of crop plants encodes insecticidal crystal 3
XX Bacillus thuringiensis delta-endotoxin.
XX
XX Disclosure; Col 105-110; 107pp; English.
XX
XX The invention relates to a modified polynucleotide which encodes an
XX insecticidal crystal 3 (Cry3) Bacillus thuringiensis delta-endotoxin such
XX as CryBb. The modified polynucleotide is useful for producing a
XX transformed cell, by introducing the modified polynucleotide into a cell
XX such as a plant cell (preferably a maize cell) or a microbial cell. The
XX modified polynucleotide is useful for producing a transformed maize plant
XX by introducing the modified polynucleotide into a maize plant cell,
XX selecting a transformed maize plant cell and regenerating a maize plant
XX from the transformed maize plant cell. A transgenic plant expressing the
XX modified polynucleotide is useful for controlling Coleopteran insect
XX infestation in a field of crop plants. The modified polynucleotide is
XX useful for producing transgenic plants expressing higher levels of the
XX insect controlling B. thuringiensis delta-endotoxin. The modified
XX polynucleotide provides up to 10 fold higher levels of insect controlling
```

CC delta-endotoxin relative to the highest levels obtained using prior
CC compositions. In particular, transgenic maize expressing higher levels of
CC the Cry3Bb protein designed to exhibit increased toxicity toward
CC Coleopteran pests deliver superior levels of insect protection and are
CC less likely to sponsor development of populations of target insects that
CC are resistant to the insecticidally active protein. Improved control of
CC susceptible target insect pests and season long protection from insect
CC pathogens is achieved using the modified polynucleotide. The modified
CC polynucleotide reduces the number of transgenic events that have to be
CC screened in order to identify one which contains beneficial levels of one
CC or more insect controlling compositions. The present sequence represents
CC *Bacillus thuringiensis* delta endotoxin Cry3Bb11231 expression cassette
CC #2 DNA
XX
SQ

Sequence 3754 BP; 1030 A; 889 C; 800 G; 1035 T; 0 U; 0 Other;
Query Match 75.3%; Score 554; DB 10; Length 3754;
Best Local Similarity 94.5%; Pred. No. 6.7e-172;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

QY 116 TCTGACGTGACATTTTCACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
Db 28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 87
QY 176 CAGCTATCTGTCATTCATCAAAAGGACAGTAGAAAAAGGAGTGCGACCTACAAATGCC 235
Db 88 CAGCTATCTGTCATTTATTGTGAAGATAGTGGNAAAGGAGTGCGTCTCTACAAATGCC 147
QY 236 ATCATTCGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGACAGTGGTCCCAAAG 295
Db 148 ATCATTCGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGACAGTGGTCCCAAAG 207
QY 296 ATGACACCCACCACGAGGAGCATCTGGAAGAGAGCTTCCAAACACGCTCTTCAA 355
Db 208 ATGACACCCACCACGAGGAGCATCTGGAAGAGAGCTTCCAAACACGCTCTTCAA 267
QY 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db 268 AGCAAGTGGATTGATGTGATGTGCTCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 327
QY 412 AACCTCTCGGATTCATTTGCCAGCTATCTGTACATTCATCAAAAGGACAGTAGAAAG 471
Db 328 AACCTCTCGGATTCATTTGCCAGCTATCTGTACATTTATTGTGAAGATAGTGGAAAG 387
QY 472 GAGGTGGCCCTCAATGCCATTCATTCGATTAAGAGAGGCTATCGTTCAGATGCC 531
Db 388 GAGGTGGCTCCTACAAATGCCATCATTTGGGATAAGGAAAGGCCATCGTTGAAGATGCC 447
QY 532 TCTGCCGACAGTGGTCCCAAAGATGGACCCACCACGAGGAGCATCGTGGAAAAAGAA 591
Db 448 TCTGCCGACAGTGGTCCCAAAGATGGACCCACCACGAGGAGCATCGTGGAAAAAGAA 507
QY 592 GACGTTCCAAACCGCTTTTCAAGCAAGTGGATGTGATATCTCCATCGACGTAAG 651
Db 508 GACGTTCCAAACCGCTTTTCAAGCAAGTGGATGTGATATCTCCATCGACGTAAG 567
QY 652 GATGACGCAATCCCACTATCTTCCGAGACCTTCTCTATATGAAGAGTTCATTT 711
Db 568 GATGACGCAATCCCACTATCTTCCGAGACCTTCTCTATATGAAGAGTTCATTT 627
QY 712 CATTTGGAGAGGACACGCTG 731
Db 628 CATTTGGAGAGGACACGCTG 647

RESULT 14
ADK98488
ID ADK98488 standard; DNA; 5170 BP.
XX
AC ADK98488;
XX
XX 03-JUN-2004 (first entry)
DT
XX

DE *B thuringiensis* cry1Bb-related expression cassette DNA SeqID11.
XX insecticidal protein; plant; pesticide; gene therapy;
KW lepidopteran insect pest; transgenic plant;
KW insect infestation resistance; monocol; dicot; cry1Bb; gene; ds.
XX
OS *Bacillus thuringiensis*.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH CDS 1241..4933
FT /tag= a
FT /product= "B thuringiensis cry1Bb variant protein"
XX
XX WO2004020636-A1.
XX
XX 11-MAR-2004.
XX
XX 26-AUG-2003; 2003WO-US026510.
XX
XX 29-AUG-2002; 2002US-0407428P.
XX
XX (MONS) MONSANTO TECHNOLOGY LLC.
PA (BOGD/) BOGDANOVA N N.
PA (ROMA/) ROMANO C P.
XX
XX Bogdanova NN, Romano CP;
XX
XX WPI; 2004-269221/25.
DR P-PSDB; ADK98489.
DR
XX
XX New polynucleotide sequence optimized for expression of an insecticidal
PT protein in a plant, useful in the control of Lepidoptera insect pests,
PT and for producing transgenic plants with the ability to resist insect
PT infestations.
XX
XX Claim 1; SEQ ID NO 11; 138pp; English.
XX
XX This invention relates to a novel polynucleotide sequence optimised for
CC expression of an insecticidal protein in a plant. The invention may be
CC useful for the production of pesticides whilst the disclosed sequences
CC may be used for gene therapy. The polynucleotide sequence and methods are
CC useful in the control of lepidopteran insect pests, and for producing
CC transgenic plants with the ability to resist insect infestations. The
CC invention provides polynucleotide sequences with enhanced, improved and
CC optimised expression in monocol and dicot plant species. The present
CC sequence is that of a B thuringiensis cry1Bb expression cassette which is
CC related to the invention.
XX
XX SQ Sequence 5170 BP; 1089 A; 1761 C; 1339 G; 981 T; 0 U; 0 Other;

Query Match 75.3%; Score 554; DB 12; Length 5170;
Best Local Similarity 94.5%; Pred. No. 7.8e-172;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

QY 116 TCTGACGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
Db 28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 87
QY 176 CAGCTATCTGTCATTCATCAAAAGGACAGTAGAAAAAGGAGTGCGACCTACAAATGCC 235
Db 88 CAGCTATCTGTCATTTATTGTGAAGATAGTGGAAAAAGGAGTGCGTCTCTACAAATGCC 147
QY 236 ATCATTCGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGACAGTGGTCCCAAAG 295
Db 148 ATCATTCGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGACAGTGGTCCCAAAG 207
QY 296 ATGACACCCACCACGAGGAGCATCTGGAAGAGAGCTTCCAAACACGCTCTTCAA 355
Db 208 ATGACACCCACCACGAGGAGCATCTGGAAGAGAGCTTCCAAACACGCTCTTCAA 267
QY 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
|||||

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 09:22:38 ; Search time 182 Seconds
(without alignments)
6617.031 Million cell updates/sec

Title: US-10-075-105C-1
Perfect score: 736
Sequence: 1 ggatccagcgtgtcctctcc.....ggagagacacgttgatcc 736

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA.*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	554	75.3	661	3	US-09-027-998A-33
2	554	75.3	2107	3	US-09-441-340-29
3	554	75.3	2122	3	US-09-441-340-25
4	554	75.3	2436	3	US-09-441-340-31
5	554	75.3	3469	4	US-09-377-466B-23
6	554	75.3	3754	4	US-09-377-466B-15
7	554	75.3	8012	3	US-09-182-117-1
8	554	75.3	8012	4	US-09-434-039A-1
9	554	75.3	8349	4	US-09-186-002-16
10	554	75.3	8418	3	US-09-182-117-5
11	554	75.3	8418	4	US-09-434-039A-5
12	554	75.3	8798	3	US-09-182-117-4
13	554	75.3	8798	4	US-09-434-039A-4
14	551.4	74.9	1030	1	US-07-936-183-46
15	551.4	74.9	1030	3	US-08-729-601A-43
16	551.4	74.9	1196	3	US-08-729-601A-46
17	551.4	74.9	5897	3	US-09-097-319A-26
18	551.4	74.9	5897	4	US-09-643-971-26
19	550.4	74.8	9335	3	US-09-097-319A-19
20	550.4	74.8	9335	4	US-09-643-971-19
21	550	74.7	10249	4	US-09-186-002-14
22	550	74.7	10339	4	US-09-186-002-13
23	548.4	74.5	10160	3	US-09-097-319A-8
24	548.4	74.5	10160	4	US-09-643-971-8
25	548.4	74.5	11784	3	US-09-097-319A-9
26	548.4	74.5	11784	4	US-09-643-971-9
27	548.4	74.5	11991	3	US-09-097-319A-10

28	548.4	74.5	11991	4	US-09-643-971-10	Sequence 10, Appl
29	543.6	73.9	4149	4	US-09-377-466B-13	Sequence 13, Appl
30	534.6	72.6	5767	4	US-09-810-861B-3	Sequence 3, Appl
31	534.6	72.6	14446	4	US-09-810-861B-4	Sequence 4, Appl
32	526	71.5	12614	4	US-09-577-424-1	Sequence 1, Appl
33	514.4	69.9	10252	4	US-09-186-002-15	Sequence 15, Appl
34	505.6	68.7	5033	1	US-08-038-768A-1	Sequence 1, Appl
35	476.8	64.8	2728	3	US-08-836-402B-7	Sequence 7, Appl
36	459.2	62.4	1138	3	US-09-011-151-8	Sequence 8, Appl
37	459.2	62.4	1138	3	US-09-011-151-9	Sequence 9, Appl
38	459	62.4	1742	3	US-09-737-698B-30	Sequence 30, Appl
39	459	62.4	1742	4	US-09-737-626A-30	Sequence 30, Appl
40	459	62.4	1800	3	US-09-737-698B-29	Sequence 29, Appl
41	459	62.4	1800	4	US-09-737-626A-29	Sequence 29, Appl
42	366	49.7	907	4	US-09-623-551-17	Sequence 17, Appl
43	351.8	47.8	978	1	US-08-446-486-31	Sequence 31, Appl
44	351.8	47.8	978	1	US-08-463-308-31	Sequence 31, Appl
45	351.8	47.8	979	1	US-08-446-486-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-09-027-998A-33
; Sequence 33, Application US/09027998A
; Patent No. 6284949
; GENERAL INFORMATION:
; APPLICANT: Fischhoff, David A
; APPLICANT: Fuchs, Roy L
; APPLICANT: Perlak, Frederick J
; TITLE OF INVENTION: Insect Resistant Plants
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White and Durkee
; STREET: PO Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,998A
; FILING DATE: 23-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Patterson, Melinda L
; REGISTRATION NUMBER: 33,062
; REFERENCE/DOCKET NUMBER: MOBT:195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 787-1400
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 661 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-027-998A-33

Query Match	75.3%;	Score 554;	DB 3;	Length 661;
Best Local Similarity	94.5%;	Pred. No. 7.8e-178;		
Matches 586;	Conservative 0;	Mismatches 30;	Indels 4;	Gaps 1;
Oy	116	TCTCAGTGAGACATTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCATTGCC	175	
Db	20	TCCGATGTGAGACATTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCATTGCC	79	
Oy	176	CAGTATCTGTCTTCATTCATAAAGGACAGTAGAAAAGGAGGTGGACCTTACAAATGCC	235	


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Db      80  CAGCTATCTGTCACTTTATTGTGAGATAGTGGAAAGGAAGGTGGCTCTACAATGCC 139
Qy      236 ATCAATTCGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGTGGTCCCAAAG 295
Db      140 ATCAATTCGGATAAAGGAAAGGCCATCGTTGAAGATGCTCTGCGGACAGTGGTCCCAAAG 199
Qy      296 ATGAGACCCCCACCACAGAGAGATCGTGGAAAAGGAGACGTTCCAAACCACTCTTCAA 355
Db      200 ATGAGACCCCCACCACAGAGAGATCGTGGAAAAGGAGACGTTTCCAAACCACTCTTCAA 259
Qy      356 AGCAAGTGGATTGATGTGAT-----TGCAGTCAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db      260 AGCAAGTGGATTGATGTGATGTCGATGTCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 319
Qy      412 AACCTCTCGGATTCCCATTTGCCAGCTATCTGTCACTTCAATCAAAAGGACAGTAGAAAAG 471
Db      320 AACCTCTCGGATTCCCATTTGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 379
Qy      472 GAAGTGGACCTACAAATGCCATCATTTGCGATAAAGGAAGGCTATCGTTCAAGATGCC 531
Db      380 GAAGTGGCTCTCAAAATGCCATCATTTGCGATAAAGGAAGGCCATCGTTGAAGATGCC 439
Qy      532 TCTGCCGACAGTGGTCCCAAAGATGGACCCGCCACCGAGGAGCATCGTGGAAAAGAA 591
Db      440 TCTGCCGACAGTGGTCCCAAAGATGGACCCGCCACCGAGGAGCATCGTGGAAAAGAA 499
Qy      592 GACGTTCCAAACCACTCTTCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAG 651
Db      500 GACGTTCCAAACCACTCTTCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAG 559
Qy      652 GATGACGCACATCCCACTATCTTCCGAAGACCTTCTCTATATAAGGAAGTTCATTT 711
Db      560 GATGACGCACATCCCACTATCTTCCGAAGACCTTCTCTATATAAGGAAGTTCATTT 619
Qy      712 CATTTGGAGAGGACACGCTG 731
Db      620 CATTTGGAGAGGACACGCTG 639
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RESULT 2

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US-09-441-340-29
; Sequence 29, Application US/09441340
; Patent No. 6448476
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/09/441.340
; CURRENT FILING DATE: 1999-11-16
; EARLIER APPLICATION NUMBER: 60/108,763
; EARLIER FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 2107
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:expression
; OTHER INFORMATION: cassette comprising plant operable promoter linked
; OTHER INFORMATION: to a leader, intron, a sequence encoding an AMPA
; OTHER INFORMATION: acetyltransferase, and termination sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (26)..(590)
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (615)..(685)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (699)..(1148)
; FEATURE:
; NAME/KEY: transit_peptide
```

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; LOCATION: (1149)..(1426)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1427)..(1858)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (1869)..(2102)
US-09-441-340-29

Query Match      75.3%; Score 554; DB 3; Length 2107;
Best Local Similarity 94.5%; Pred. No. 1.5e-177;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy      116 TCTGCACTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCGATGCC 175
Db      28  TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCGATGCC 87
Qy      176 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAGGAGGCGACCTACAAATGCC 235
Db      88  CAGCTATCTGTCACTTATTGTGAAGATAGTGGAAAAGGAGGCTCTTACAAATGCC 147
Qy      236 ATCAATTCGGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGTGGTCCCAAAG 295
Db      148 ATCAATTCGGATAAAGGAAAGGCCATCGTTGAAGATGCTCTGCGGACAGTGGTCCCAAAG 207
Qy      296 ATGGACCCCCACCACGAGGAGCATCGTGGAAAAGGAGACGTTCCAAACCACTCTTCAA 355
Db      208 ATGGACCCCCACCACGAGGAGCATCGTGGAAAAGGAGACGTTCCAAACCACTCTTCAA 267
Qy      356 AGCAAGTGGATTGATGTGAT---TGCAGTCAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db      268 AGCAAGTGGATTGATGTGATGTCGATGTCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 327
Qy      412 AACCTCTCGGATTCCCATTTGCCAGCTATCTGTCACTTCAATCAAAAGGACAGTAGAAAAG 471
Db      328 AACCTCTCGGATTCCCATTTGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 387
Qy      472 GAAGTGGGACCTACAAATGCCATCATTTGCGATAAAGGAAGGCTATCGTTCAAGATGCC 531
Db      388 GAAGTGGGCTCTTACAAATGCCATCATTTGCGATAAAGGAAGGCCATCGTTGAAGATGCC 447
Qy      532 TCTGCCGACAGTGGTCCCAAAGATGGACCCGCCACCGAGGAGCATCGTGGAAAAGAA 591
Db      448 TCTGCCGACAGTGGTCCCAAAGATGGACCCGCCACCGAGGAGCATCGTGGAAAAGAA 507
Qy      592 GACGTTCCAAACCACTCTTCAAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAG 651
Db      508 GACGTTCCAAACCACTCTTCAAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAG 567
Qy      652 GATGACGCACAAATCCCACTATCTTCCGAAGACCTTCTCTATATAAGGAAGTTCATTT 711
Db      568 GATGACGCACAAATCCCACTATCTTCCGAAGACCTTCTCTATATAAGGAAGTTCATTT 627
Qy      712 CATTTGGAGAGGACACGCTG 731
Db      628 CATTTGGAGAGGACACGCTG 647
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RESULT 3

```
US-09-441-340-25
; Sequence 25, Application US/09441340
; Patent No. 6448476
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/09/441.340
; CURRENT FILING DATE: 1999-11-16
; EARLIER APPLICATION NUMBER: 60/108,763
; EARLIER FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
```

```

; LENGTH: 2122
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; OTHER INFORMATION: cassette comprising plant promoter linked to
; OTHER INFORMATION: sequence encoding AMPA acetyl transferase linked
; OTHER INFORMATION: to termination sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (6)..(620)
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (645)..(715)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (729)..(1178)
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1179)..(1406)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1407)..(1838)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (1849)..(2082)
US-09-441-340-25

Query Match 75.3%; Score 554; DB 3; Length 2122;
Best Local Similarity 94.5%; Pred. No. 1.5e-177;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCGATTGCC 175
Db 8 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCGATTGCC 67

Qy 176 CAGCTATCTGTCACCTTATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCC 235
Db 68 CAGCTATCTGTCACCTTATTTGGAAGATAGTGGAAAAGGAAGGTGGCTCTTACAAATGCC 127

Qy 236 ATCATTCGGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAG 295
Db 128 ATCATTCGGATAAAGGAAGGCACTCGTTGAAGATGCTCTGCCGACAGTGGTCCCAAG 187

Qy 296 ATGGACCCACCCACGAGGAGCATCGTGGAAAAGGAAGAGCTTCCAAACACGCTTCAA 355
Db 188 ATGGACCCACCCACGAGGAGCATCGTGGAAAAGGAAGAGCTTCCAAACACGCTTCAA 247

Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGA 411
Db 248 AGCAAGTGGATTGATGTGATGTGCGATGTGAGACTTTTCAACAAAGGGTAATATCGGA 307

Qy 412 AACCTCTCGGATTCGATTCGCGAGCTATCTGTCATTCATCAAAAGGACAGTAGAAAAG 471
Db 308 AACCTCTCGGATTCGATTCGCGAGCTATCTGTCATTCATTCGGAAGATAGTGGAAAAG 367

Qy 472 GAAGTGGCACCTACAAATGCCATCATTTGGCATAAAGGAAGGCTATCGTTCAAGATGCC 531
Db 368 GAAGTGGCTCTTACAAATGCCATCATTTGGCATAAAGGAAGGCTATCGTTGAAGATGCC 427

Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCACCCACGAGGAGCATCGTGGAAAAGAA 591
Db 428 TCTGCCGACAGTGGTCCCAAGATGGACCCACCCACGAGGAGCATCGTGGAAAAGAA 487

Qy 592 GACGTTCCAAACGCTCTTCAAGCAAGTGGATGATGATGATATCTCACTGACGTAAAG 651
Db 488 GACGTTCCAAACGCTCTTCAAGCAAGTGGATGATGATGATATCTCACTGACGTAAAG 547

Qy 652 GATGACGACAAATCCCACTATCTTCGCAAGACCCCTCTCTATATAAGGAAGTTCATTT 711
Db 548 GATGACGACAAATCCCACTATCTTCGCAAGACCCCTCTCTATATAAGGAAGTTCATTT 607

Qy 712 CATTGGAGAGGACACGCTG 731
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Db 608 CATTGGAGAGGACACGCTG 627

RESULT 4
US-09-441-340-31
; Sequence 31, Application US/09441340
; Patent No. 6448476
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/09/441.340
; CURRENT FILING DATE: 1999-11-16
; EARLIER APPLICATION NUMBER: 60/108,763
; EARLIER FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: monocot
; OTHER INFORMATION: expression cassette comprising plant operable
; OTHER INFORMATION: promoter linked to an intron, a sequence coding
; OTHER INFORMATION: for an AMPA acetyltransferase, and a termination
; OTHER INFORMATION: sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (26)..(640)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (670)..(1473)
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1498)..(1725)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1726)..(2157)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (2172)..(2427)
US-09-441-340-31
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Query Match 75.3%; Score 554; DB 3; Length 2436;
Best Local Similarity 94.5%; Pred. No. 1.6e-177;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCGATTGCC 175
Db 28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCGATTGCC 87

Qy 176 CAGCTATCTGTCACCTTATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCC 235
Db 88 CAGCTATCTGTCACCTTATTTGGAAGATAGTGGAAAAGGAAGGTGGCTCTTACAAATGCC 147

Qy 236 ATCATTCGGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAG 295
Db 148 ATCATTCGGATAAAGGAAGGCTATCGTTGAAGATGCTCTGCCGACAGTGGTCCCAAG 207

Qy 296 ATGGACCCACCCACGAGGAGCATCGTGGAAAAGGAAGAGCTTCCAAACACGCTTCAA 355
Db 208 ATGGACCCACCCACGAGGAGCATCGTGGAAAAGGAAGAGCTTCCAAACACGCTTCAA 267

Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGA 411
Db 268 AGCAAGTGGATTGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 327

Qy 412 AACCTCTCGGATTCGATTCGCGAGCTATCTGTCATTCATCAAAAGGACAGTAGAAAAG 471
Db 328 AACCTCTCGGATTCGATTCGCGAGCTATCTGTCATTCATTCATTCATTCATTCATTCATTC 387
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Db 28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGAACCTCTCCGATTCCATTGCC 87
Qy 176 CAGCTATCTGTCTACATTCATAAAGGACAGTAGAAAAGGAGGCGCACCTACAAATGCC 235
Db 88 CAGCTATCTGTCTACATTCATAAAGGACAGTAGAAAAGGAGGCGCTCTACAAATGCC 147
Qy 236 ATCATTTGGATTAAGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGTAGTGGTCCCAAG 295
Db 148 ATCATTTGGATTAAGAAAGGCGCTATCGTTCAAGATGCTCTGCGGACAGTAGTGGTCCCAAG 207
Qy 296 ATGGACCCCCACCCAGGAGGAGCTGTTGGAAGAAAGAGAGGTTCCAAACACAGCTCTTCAA 355
Db 208 ATGGACCCCCACCCAGGAGGAGCTGTTGGAAGAAAGAGAGGTTCCAAACACAGCTCTTCAA 267
Qy 356 AGCAAGTGGATTGATGTCAT----TGCAAGTGGAGCTTTTCAACAAAGGGTAATATCCGGA 411
Db 268 AGCAAGTGGATTGATGTCATGTCGTCGATGTCGAGACTTTTCAACAAAGGGTAATATCCGGA 327
Qy 412 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 471
Db 328 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 387
Qy 472 GAAGTGGCAGCTACAAATGCCATCATTTGCGATAAAGGAGGCTATCGTTCAAGATGCC 531
Db 388 GAAGTGGCTCTACAAATGCCATCATTTGCGATAAAGGAGGCGCTATCGTTGAAGATGCC 447
Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCACCCAGGAGGAGCATCGTGGAAAAGAA 591
Db 448 TCTGCCGACAGTGGTCCCAAGATGGACCCACCCAGGAGGAGCATCGTGGAAAAGAA 507
Qy 592 GACGTTCCAAACAGCTCTTTCAAGCAAGTGGATTGATGTAATCTCACTGACGTAAAG 651
Db 508 GACGTTCCAAACAGCTCTTTCAAGCAAGTGGATTGATGTAATCTCACTGACGTAAAG 567
Qy 652 GATGAGCAGCAATCCCACTATCTTCCGACAGCCTTCTCTATATAGGAAGTTCATTT 711
Db 568 GATGAGCAGCAATCCCACTATCTTCCGACAGCCTTCTCTATATAGGAAGTTCATTT 627
Qy 712 CATTTGGAGAGGACACGCTG 731
Db 628 CATTTGGAGAGGACACGCTG 647

RESULT 7

US-09-182-117-1
; Sequence 1, Application US/09182117
; Patent No. 6204436
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic Plant
; NUMBER OF SEQUENCES: 27
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/182,117
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8012 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-182-117-1

Query Match 75.3%; Score 554; DB 3; Length 8012;
Best Local Similarity 94.5%; Pred. No. 3.3e-177;

Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
Qy 116 TCTCAGTGAAGACTTTTCAACAAAGGGTAATATCGGAAAACCTCTCCGATTCCATTGCC 175
Db 3044 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAAACCTCTCTCGGATTCCATTGCC 3103
Qy 176 CAGCTATCTGTCTACATTCATAAAGGACAGTAGAAAAGGAGGCGCACCTACAAATGCC 235
Db 3104 CAGCTATCTGTCTACATTCATAAAGGACAGTAGAAAAGGAGGCGCTCTACAAATGCC 3163
Qy 236 ATCATTTGGATTAAGAAAGGCTATCGTTCAAGATGCTCTGCGGACAGTAGTGGTCCCAAG 295
Db 3164 ATCATTTGGATTAAGAAAGGCGCTATCGTTCAAGATGCTCTGCGGACAGTAGTGGTCCCAAG 3223
Qy 296 ATGGACCCCCACCCAGGAGGAGCTGTTGGAAGAAAGAGAGGTTCCAAACACAGCTCTTCAA 355
Db 3224 ATGGACCCCCACCCAGGAGGAGCTGTTGGAAGAAAGAGAGGTTCCAAACACAGCTCTTCAA 3283
Qy 356 AGCAAGTGGATTGATGTCAT----TGCAAGTGGAGCTTTTCAACAAAGGGTAATATCCGGA 411
Db 3284 AGCAAGTGGATTGATGTCATGTCGTCGATGTCGAGACTTTTCAACAAAGGGTAATATCCGGA 3343
Qy 412 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 471
Db 3344 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 3403
Qy 472 GAAGTGGCAGCTACAAATGCCATCATTTGCGATAAAGGAGGCTATCGTTCAAGATGCC 531
Db 3404 GAAGTGGCTCTTACAAATGCCATCATTTGCGATAAAGGAGGCGCTATCGTTGAAGATGCC 3463
Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCACCCAGGAGGAGCATCGTGGAAAAGAA 591
Db 3464 TCTGCCGACAGTGGTCCCAAGATGGACCCACCCAGGAGGAGCATCGTGGAAAAGAA 3523
Qy 592 GACGTTCCAAACAGCTCTTCAAGCAAGTGGATTGATGTAATCTCACTGACGTAAAG 651
Db 3524 GACGTTCCAAACAGCTCTTCAAGCAAGTGGATTGATGTAATCTCACTGACGTAAAG 3583
Qy 652 GATGAGCAGCAATCCCACTATCTTCCGACAGCCTTCTCTATATAGGAAGTTCATTT 711
Db 3584 GATGAGCAGCAATCCCACTATCTTCCGACAGCCTTCTCTATATAGGAAGTTCATTT 3643
Qy 712 CATTTGGAGAGGACACGCTG 731
Db 3644 CATTTGGAGAGGACACGCTG 3663

RESULT 8

US-09-434-039A-1
; Sequence 1, Application US/09434039A
; Patent No. 6531649
; GENERAL INFORMATION:
; APPLICANT: MANNERLOEF, Marie
; APPLICANT: TENNING, Paul Peter
; APPLICANT: STEEN, Per
; TITLE OF INVENTION: Transgenic Plants
; FILE REFERENCE: 09/434,039
; CURRENT APPLICATION NUMBER: US/09/434,039A
; CURRENT FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/112,003
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 09/182,117
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 8012
; TYPE: DNA
; ORGANISM: Sugar beet
US-09-434-039A-1

Query Match 75.3%; Score 554; DB 4; Length 8012;
Best Local Similarity 94.5%; Pred. No. 3.3e-177;

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Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
Qy 116 TCTGAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 175
Db 3044 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 3103
Qy 176 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAGGAGGTGGCACCCTACAAATGCC 235
Db 3104 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAGGAGGTGGTCTCTACAAATGCC 3163
Qy 236 ATCAATTCGATAAAGGAAAGCTATCGTTCAAGATGCTCTGCGCAGCAGTGGTCCCAAAG 295
Db 3164 ATCAATTCGATAAAGGAAAGGCCATCGTTGAAGATGCTCTGCGCAGCAGTGGTCCCAAAG 3223
Qy 296 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAGAGCTTCCAAACACGCTCTTCAA 355
Db 3224 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAGAGCTTCCAAACACGCTCTTCAA 3283
Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db 3284 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 3343
Qy 412 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAG 471
Db 3344 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAG 3403
Qy 472 GAAGGTGGCACCACCAATGCCATCATTCGATTAAGAAAGGAGCTATCGTTCAAGATGCC 531
Db 3404 GAAGGTGGCTCTCAAAATGCCATCATTCGATTAAGAAAGGAGCTATCGTTCAAGATGCC 3463
Qy 532 TCTGCCGACAGTGGTCCAAAGATGGACCCGCCACGAGGAGCATCGTGGAAAAAGAA 591
Db 3464 TCTGCCGACAGTGGTCCAAAGATGGACCCGCCACGAGGAGCATCGTGGAAAAAGAA 3523
Qy 592 GACGTTCCAAACCACTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAG 651
Db 3524 GACGTTCCAAACCACTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAG 3583
Qy 652 GATGACGCACAAATCCCACTATCTTCCGAAAGCCCTCTCTATATAAGGAAGTTCAATTT 711
Db 3584 GATGACGCACAAATCCCACTATCTTCCGAAAGCCCTCTCTATATAAGGAAGTTCAATTT 3643
Qy 712 CATTTGGAGAGGACACGCTG 731
Db 3644 CATTTGGAGAGGACACGCTG 3663
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RESULT 9
US-09-186-002-16
; Sequence 16, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, Charles P.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
; CURRENT APPLICATION NUMBER: US/09/186,002B
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 8349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (3666)..(5573)
; OTHER INFORMATION: completely synthesized
US-09-186-002-16
Query Match 75.3%; Score 554; DB 4; Length 8349;
Best Local Similarity 94.5%; Pred. No. 3.3e-177;
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Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
Qy 116 TCTGAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 175
Db 1807 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 1866
Qy 176 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAGGAGGTGGCACCCTACAAATGCC 235
Db 1867 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAGGAGGTGGTCTCTACAAATGCC 1926
Qy 236 ATCAATTCGATAAAGGAAAGCTATCGTTCAAGATGCTCTGCGCAGCAGTGGTCCCAAAG 295
Db 1927 ATCAATTCGATAAAGGAAAGGCCATCGTTGAAGATGCTCTGCGCAGCAGTGGTCCCAAAG 1986
Qy 296 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAGAGCTTCCAAACACGCTCTTCAA 355
Db 1987 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAGAGCTTCCAAACACGCTCTTCAA 2046
Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db 2047 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 2106
Qy 412 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAG 471
Db 2107 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAG 2166
Qy 472 GAAGGTGGCACCCTACAAATGCCATCATTCGATTAAGAAAGGAGCTATCGTTCAAGATGCC 531
Db 2167 GAAGGTGGCTCTCAAAATGCCATCATTCGATTAAGAAAGGAGCTATCGTTCAAGATGCC 2226
Qy 532 TCTGCCGACAGTGGTCCAAAGATGGACCCGCCACGAGGAGCATCGTGGAAAAAGAA 591
Db 2227 TCTGCCGACAGTGGTCCAAAGATGGACCCGCCACGAGGAGCATCGTGGAAAAAGAA 2286
Qy 592 GACGTTCCAAACCACTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAG 651
Db 2287 GACGTTCCAAACCACTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAG 2346
Qy 652 GATGACGCACAAATCCCACTATCTTCCGAAAGCCCTCTCTATATAAGGAAGTTCAATTT 711
Db 2347 GATGACGCACAAATCCCACTATCTTCCGAAAGCCCTCTCTATATAAGGAAGTTCAATTT 2406
Qy 712 CATTTGGAGAGGACACGCTG 731
Db 2407 CATTTGGAGAGGACACGCTG 2426
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RESULT 10
US-09-182-117-5
; Sequence 5, Application US/09182117
; Patent No. 6204436
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic Plant
; NUMBER OF SEQUENCES: 27
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/182,117
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8418 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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US-09-182-117-4
US-09-182-117-4
Sequence 4, Application US/09182117
Patent No. 6204436
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Transgenic Plant
NUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/182,117
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8798 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-182-117-4

Query Match      75.3%; Score 554; DB 3; Length 8798;
Best Local Similarity 94.5%; Pred. No. 3.4e-177;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTCAGTGAGACATTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 175
Db 3133 TCCGATGTGAGACATTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 3192

Qy 176 CAGCTATCTGTCTCATCTTCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCC 235
Db 3193 CAGCTATCTGTCTCATCTTCAAAAGGACAGTAGAAAAGGAAGGTGGCTCTTACAAATGCC 3252

Qy 236 ATCAATTGCGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 295
Db 3253 ATCAATTGCGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 3312

Qy 296 ATGACACCCCAACCCACGAGGAGCATCGTGGAAAAGGAAGACGTTTCCAAACCAAGTCTTCAA 355
Db 3313 ATGACACCCCAACCCACGAGGAGCATCGTGGAAAAGGAAGACGTTTCCAAACCAAGTCTTCAA 3372

Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGTAATATCGGGA 411
Db 3373 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGTAATATCGGGA 3432

Qy 412 AACCTCTCGGATTTCCATTTGCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAG 471
Db 3433 AACCTCTCGGATTTCCATTTGCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAG 3492

Qy 472 GAAGGTGGACCTACAAATGCCATTCATTCGATATAAGAAAGGCTATCGTTCAAGATGCC 531
Db 3493 GAAGGTGGCTCTCAAAATGCCATTCATTCGATATAAGAAAGGCTATCGTTCAAGATGCC 3552

Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAGAA 591
Db 3553 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAGAA 3612

Qy 592 GACGTTTCCAAACCAAGTCTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG 651
Db 3613 GACGTTTCCAAACCAAGTCTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG 3672

Qy 652 GATGACGACAAATCCCACTATCTTTCGCAAGACCCCTTCTCTATATAAGGAAGTTCATTT 711
Db 3673 GATGACGACAAATCCCACTATCTTTCGCAAGACCCCTTCTCTATATAAGGAAGTTCATTT 3732

Qy 712 CATTTGGAGGACACGCTG 731
Db 3733 CATTTGGAGGACACGCTG 3752
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RESULT 13
US-09-434-039A-4
; Sequence 4, Application US/09434039A
; Patent No. 6531649
; GENERAL INFORMATION:
; APPLICANT: MANNERLOEF, Marie
; APPLICANT: TENNING, Paul Peter
; APPLICANT: STEEN, Per
; TITLE OF INVENTION: Transgenic Plants
; FILE REFERENCE: 09/434,039
; CURRENT APPLICATION NUMBER: US/09/434,039A
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/112,003
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 09/182,117
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 4
; LENGTH: 8798
; TYPE: DNA
; ORGANISM: Sugar beet
US-09-434-039A-4

Query Match      75.3%; Score 554; DB 4; Length 8798;
Best Local Similarity 94.5%; Pred. No. 3.4e-177;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTCAGTGAGACATTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 175
Db 3133 TCCGATGTGAGACATTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 3192

Qy 176 CAGCTATCTGTCTCATCTTCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCC 235
Db 3193 CAGCTATCTGTCTCATCTTCAAAAGGACAGTAGAAAAGGAAGGTGGCTCTTACAAATGCC 3252

Qy 236 ATCAATTGCGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 295
Db 3253 ATCAATTGCGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 3312

Qy 296 ATGACACCCCAACCCACGAGGAGCATCGTGGAAAAGGAAGACGTTTCCAAACCAAGTCTTCAA 355
Db 3313 ATGACACCCCAACCCACGAGGAGCATCGTGGAAAAGGAAGACGTTTCCAAACCAAGTCTTCAA 3372

Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGTAATATCGGGA 411
Db 3373 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGTAATATCGGGA 3432

Qy 412 AACCTCTCGGATTTCCATTTGCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAG 471
Db 3433 AACCTCTCGGATTTCCATTTGCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAG 3492

Qy 472 GAAGGTGGACCTACAAATGCCATTCATTCGATATAAGAAAGGCTATCGTTCAAGATGCC 531
Db 3493 GAAGGTGGCTCTCAAAATGCCATTCATTCGATATAAGAAAGGCTATCGTTCAAGATGCC 3552

Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAGAA 591
Db 3553 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCACGAGGAGCATCGTGGAAAAGAA 3612

Qy 592 GACGTTTCCAAACCAAGTCTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG 651
Db 3613 GACGTTTCCAAACCAAGTCTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG 3672

Qy 652 GATGACGACAAATCCCACTATCTTTCGCAAGACCCCTTCTCTATATAAGGAAGTTCATTT 711
Db 3673 GATGACGACAAATCCCACTATCTTTCGCAAGACCCCTTCTCTATATAAGGAAGTTCATTT 3732

Qy 712 CATTTGGAGGACACGCTG 731
Db 3733 CATTTGGAGGACACGCTG 3752
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RESULT 14
US-07-936-163-46
; Sequence 46, Application US/07936163
; Patent No. 5743477
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: MERLO, DONALD J
; APPLICANT: HOUTCHENS, ROBERT A
; APPLICANT: STRICKLAND, JAMES A
; APPLICANT: ORR, GREGORY L
; TITLE OF INVENTION: INSECTICIDAL PROTEINS AND METHOD FOR
; TITLE OF INVENTION: PLANT PROTECTION
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THOMAS D. ZINDRICK
; STREET: 9002 PURDUE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
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COUNTRY: US
ZIP: 46268-1189
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/936,163
FILING DATE: 27-AUG-1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: ZINDRICK, THOMAS D
REGISTRATION NUMBER: 32,185
REFERENCE/DOCKET NUMBER: C-38,424A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 636-1869
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1030 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-936-163-46

Query Match 74.9%; Score 551.4; DB 1; Length 1030;
Best Local Similarity 93.2%; Pred. No. 7.7e-177;
Matches 588; Conservative 0; Mismatches 41; Indels 2; Gaps 1;

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Qy 105 CTGCAGAGCTTCTGCAGTGAGACTTTTCAACAAGGGTAAATATCGGGAACCTCTCGG 164
Db 13 CTGCAGATCTGCATGGTGGAGACTTTTCAACAAGGGTAAATATCGGGAACCTCTCGG 72
Qy 165 ATTCATTTGCCAGTCTCTGCTACTTCTCATCAAAAGGACAGTAGAGAAAGGAGTGGCAC 224
Db 73 ATTCATTTGCCAGTCTCTGCTACTTCTCATCAAAAGGACAGTAGAGAAAGGAGTGGCTC 132
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Db 133 CTACAAATGCCATCATTTGCGATAAAGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAG 192
Qy 285 TGGTCCCAAGATGGACCCCAACCCACGAGAGAGATCGTGGAAAAAGAGACGTTCCAAC 344
Db 193 TGGTCCCAAGATGGACCCCAACCCACGAGAGAGATCGTGGAAAAAGAGACGTTCCAAC 252
Qy 345 CACGTCTTTCAAGCAAGTGGATTGATGTGAT--TGCAGTGAGACTTTTCAACAAGGGTAA 402
Db 253 CACGTCTTTCAAGCAAGTGGATTGATGTGATGTGATGTGATGTGATGTGATGTGATGTG 312
Qy 403 ATATCGGAAACCTCTCGGATTCATTTGCCAGCTATCTGTCTACTTTCATCAAAAGGACA 462
Db 313 ATATCGGAAACCTCTCGGATTCATTTGCCAGCTATCTGTCTACTTTCATCAAAAGGATA 372
Qy 463 GTAGAAAAGGAGTGGACCTACAAATGCCATCATTTGCCGATAAAGAGGCTATCGTT 522
Db 373 GTGAAAAGGAGTGGGCTCTTCAAAATGCCATCATTTGCCGATAAAGAGGCTATCGTT 432
Qy 523 CAAGATGCTCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCACGAGAGAGATCGTG 582
Db 433 GAAGATGCTCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCACGAGAGAGATCGTG 492
Qy 583 GAAAAAGAGACGTTTCAACCAACGCTCTTTCAAGCAAGTGGATTGATGTGATATCTCCACT 642
Db 493 GAAAAAGAGACGTTTCAACCAACGCTCTTTCAAGCAAGTGGATTGATGTGATATCTCCACT 552
Qy 643 GACGTAGGGATGAGGCAAAATCCCATATCTCTCGGAAGACCCCTTCTCTATATAAGGA 702
Db 553 GACGTAGGGATGAGGCAAAATCCCATATCTCTCGGAAGACCCCTTCTCTATATAAGGA 612
Qy 703 AGTTTCATTTTGGAGAGGACGCTGGA 733
Db 613 AGTTTCATTTTGGAGAGAACACGGGGGA 643
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RESULT 15
US-08-729-601A-43
Sequence 43, Application US/08729601A
Patent No. 6166302
GENERAL INFORMATION:
APPLICANT: Merlo, Donald J.
APPLICANT: Folkerts, Otto
TITLE OF INVENTION: Modified Bacillus Thuringiensis Gene for
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 S. LaSalle St.
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/729,601A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Krueger, James P.
REGISTRATION NUMBER: 35,234
REFERENCE/DOCKET NUMBER: 60089
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
TELEFAX: 312-372-7848
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1030 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-729-601A-43

Query Match 74.9%; Score 551.4; DB 3; Length 1030;
Best Local Similarity 93.2%; Pred. No. 7.7e-177;
Matches 588; Conservative 0; Mismatches 41; Indels 2; Gaps 1;

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Qy 105 CTGCAGAGCTTCTGCAGTGAGACTTTTCAACAAGGGTAAATATCGGGAACCTCTCGG 164
Db 13 CTGCAGATCTGCATGGTGGAGACTTTTCAACAAGGGTAAATATCGGGAACCTCTCGG 72
Qy 165 ATTCATTTGCCAGTCTCTGCTACTTCTCATCAAAAGGACAGTAGAGAAAGGAGTGGCAC 224
Db 73 ATTCATTTGCCAGTCTCTGCTACTTCTCATCAAAAGGACAGTAGAGAAAGGAGTGGCTC 132
Qy 225 CTACAAATGCCATCATTTGCGATAAAGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAG 284
Db 133 CTACAAATGCCATCATTTGCGATAAAGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAG 192
Qy 285 TGGTCCCAAGATGGACCCCAACCCACGAGAGAGATCGTGGAAAAAGAGACGTTCCAAC 344
Db 193 TGGTCCCAAGATGGACCCCAACCCACGAGAGAGATCGTGGAAAAAGAGACGTTCCAAC 252
Qy 345 CACGTCTTTCAAGCAAGTGGATTGATGTGAT--TGCAGTGAGACTTTTCAACAAGGGTAA 402
Db 253 CACGTCTTTCAAGCAAGTGGATTGATGTGATGTGATGTGATGTGATGTGATGTGATGTG 312
Qy 403 ATATCGGAAACCTCTCGGATTCATTTGCCAGCTATCTGTCTACTTTCATCAAAAGGACA 462
Db 313 ATATCGGAAACCTCTCGGATTCATTTGCCAGCTATCTGTCTACTTTCATCAAAAGATA 372
Qy 463 GTAGAAAAGGAGTGGACCTACAAATGCCATCATTTGCCGATAAAGAGGCTATCGTT 522
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Db	373	GTGAAAAGGAAGTGGCTCTACAAATGCCATCATTTGCGATAAAGGAAGGCCATCGTT	432
Qy	523	CAAGATGCTCTGCGACAGTGTCCCAAGATGGACCCGCCACGAGGAGCATCGTG	582
Db	433	GAAGATGCTCTGCGACAGTGTCCCAAGATGGACCCGCCACGAGGAGCATCGTG	492
Qy	583	GAAAAGAAGACGTTCCAAACCACTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACT	642
Db	493	GAAAAGAAGACGTTCCAAACCACTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACT	552
Qy	643	GACGTAAGGGATGACGACACATCCCACTATCTTCGCAAGACCCCTTCTATATAAGGA	702
Db	553	GACGTAAGGGATGACGACACATCCCACTATCTTCGCAAGACCCCTTCTATATAAGGA	612
Qy	703	AGTTCAATTCATTGGAGGACACGCTGGA	733
Db	613	AGTTCAATTCATTGGAGGACACGCTGGA	643

Search completed: October 11, 2005, 14:58:23
Job time : 186 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 12:54:20 ; Search time 718 Seconds
(without alignments)
7139.448 Million cell updates/sec

Title: US-10-075-105C-1

Perfect score: 736

Sequence: 1 ggatccagcggtctctcc.....ggagaggacagctggatcc 736

Scoring table: IDENTITY NUC

Gapop 10'0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
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- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	736	100.0	736	22	US-10-075-105C-1 Sequence 1, Appli
2	597.4	81.2	1360	22	US-10-075-105C-3 Sequence 3, Appli
3	554	75.3	661	9	US-09-943-692-33 Sequence 33, Appl
4	554	75.3	2107	15	US-10-213-791-29 Sequence 29, Appl
5	554	75.3	2122	15	US-10-213-791-25 Sequence 25, Appl
6	554	75.3	2436	15	US-10-213-791-31 Sequence 31, Appl
7	554	75.3	3469	15	US-10-232-665-23 Sequence 23, Appl

8	554	75.3	3754	15	US-10-232-665-15	Sequence 15, Appl
9	554	75.3	8349	16	US-10-198-478-16	Sequence 16, Appl
c 10	551.4	74.9	5796	17	US-10-378-810-2	Sequence 2, Appli
11	551.4	74.9	5897	19	US-10-759-602-26	Sequence 26, Appl
12	550.4	74.8	9335	19	US-10-759-602-19	Sequence 19, Appl
13	550	74.7	10249	16	US-10-198-478-14	Sequence 14, Appl
14	550	74.7	10312	16	US-10-198-478-15	Sequence 15, Appl
15	550	74.7	10339	16	US-10-198-478-13	Sequence 13, Appl
16	548.4	74.5	10160	19	US-10-759-602-8	Sequence 8, Appli
17	548.4	74.5	11784	19	US-10-759-602-9	Sequence 9, Appli
18	548.4	74.5	11991	19	US-10-759-602-10	Sequence 10, Appl
19	543.6	73.9	4149	15	US-10-232-665-13	Sequence 13, Appl
20	534.6	72.6	5767	9	US-09-810-861B-3	Sequence 3, Appli
21	534.6	72.6	5767	22	US-10-792-491-3	Sequence 3, Appli
22	534.6	72.6	14446	9	US-09-810-861B-4	Sequence 4, Appli
23	534.6	72.6	14446	22	US-10-792-491-4	Sequence 4, Appli
24	526	71.5	829	14	US-10-109-812-10	Sequence 10, Appl
25	526	71.5	1334	16	US-10-322-656-12	Sequence 12, Appl
c 26	526	71.5	11478	21	US-10-473-945-2	Sequence 2, Appli
27	526	71.5	12304	21	US-10-473-945-5	Sequence 5, Appli
c 28	526	71.5	12497	21	US-10-473-945-4	Sequence 4, Appli
c 29	514	69.8	8428	15	US-10-161-403-90	Sequence 90, Appl
c 30	514	69.8	8428	20	US-10-161-408-2	Sequence 2, Appli
c 31	514	69.8	8428	24	US-11-006-076-90	Sequence 90, Appl
c 32	514	69.8	10122	15	US-10-161-403-97	Sequence 97, Appl
c 33	514	69.8	10122	20	US-10-161-408-8	Sequence 8, Appli
c 34	514	69.8	10122	24	US-11-006-076-97	Sequence 97, Appl
c 35	514	69.8	10549	15	US-10-161-403-92	Sequence 92, Appl
c 36	514	69.8	10549	20	US-10-161-408-3	Sequence 3, Appli
c 37	514	69.8	10549	24	US-11-006-076-92	Sequence 92, Appl
c 38	514	69.8	11182	15	US-10-161-403-89	Sequence 89, Appl
c 39	514	69.8	11182	15	US-10-161-403-89	Sequence 89, Appl
c 40	514	69.8	11182	20	US-10-161-408-1	Sequence 1, Appli
c 41	514	69.8	11182	20	US-10-161-408-1	Sequence 1, Appli
c 42	514	69.8	11182	24	US-11-006-076-89	Sequence 89, Appl
c 43	514	69.8	11182	24	US-11-006-076-89	Sequence 89, Appl
c 44	514	69.8	12592	15	US-10-161-403-95	Sequence 95, Appl
c 45	514	69.8	12592	15	US-10-161-403-95	Sequence 95, Appl

ALIGNMENTS

RESULT 1

US-10-075-105C-1
; Sequence 1, Application US/10075105C
; Publication No. US20050188432A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zhijian T
; TITLE OF INVENTION: Bi-Directional Dual Promoter Complex with Enhanced Promoter Activ
; TITLE OF INVENTION: Transgene Expression in Eukaryotes
; FILE REFERENCE: 7270-72978
; CURRENT APPLICATION NUMBER: US/10/075.105C
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 60/268,358
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 736
; TYPE: DNA
; ORGANISM: CamV 35S
; FEATURE:
; OTHER INFORMATION:
US-10-075-105C-1

Query Match 100.0%; Score 736; DB 22; Length 736;
Best Local Similarity 100.0%; Pred. No. 1.5e-238;
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATCCAGCGTCTCTCCAAATGAATGAATCTTATATAGAGAGGGTCTTCCG 60

Db 1 GGATCCAGCGTCTCTCCAAATGAAATGAATCTTCTTATATAGAGGAAGGTCCTTGGC 60
Qy 61 AAGGATAGTGGGATTGTGGCTCATCTCCCTTACGTTCAGTGGAGATACCTGCAAGCTTCTGC 120
Db 61 AAGGATAGTGGGATTGTGGCTCATCTCCCTTACGTTCAGTGGAGATACCTGCAAGCTTCTGC 120
Qy 121 AGTGAGACTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCCATTGCCCCAGCT 180
Db 121 AGTGAGACTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCCATTGCCCCAGCT 180
Qy 181 ATCTGTCACTTCATCAAAAGGACAGTAGAAGAAAGAGGTCGCACCTACAAATGCCATCAT 240
Db 181 ATCTGTCACTTCATCAAAAGGACAGTAGAAGAAAGAGGTCGCACCTACAAATGCCATCAT 240
Qy 241 TGGGATTAAGGAAGGCTATCGTTCAAGATGCCTCTGCCACAGTGTCTCCAAAGATGGA 300
Db 241 TGGGATTAAGGAAGGCTATCGTTCAAGATGCCTCTGCCACAGTGTCTCCAAAGATGGA 300
Qy 301 CCCCCACCCAGGAGCATCGTGGAAAAAGAGAGCTTCCAAACAGTCTTCAAAAGCAA 360
Db 301 CCCCCACCCAGGAGCATCGTGGAAAAAGAGAGCTTCCAAACAGTCTTCAAAAGCAA 360
Qy 361 GTGGATTGATGTGATTCGAGTGAGACTTTTCAACAAAGGTAATATCGGGAACCTCTCTC 420
Db 361 GTGGATTGATGTGATTCGAGTGAGACTTTTCAACAAAGGTAATATCGGGAACCTCTCTC 420
Qy 421 GGATTTCATTGCCAGCTATCTGTCACTTCATCAAAAGGTAATATCGGGAACCTCTCTC 480
Db 421 GGATTTCATTGCCAGCTATCTGTCACTTCATCAAAAGGTAATATCGGGAACCTCTCTC 480
Qy 481 ACCTACAAATGCCATCATTCGGATAAAGAAAGGCTATCGTTCAAGATGCCTCTGCCGAC 540
Db 481 ACCTACAAATGCCATCATTCGGATAAAGAAAGGCTATCGTTCAAGATGCCTCTGCCGAC 540
Qy 541 AGTGGTCCCCAAGATGACCCCCACCCACGAGGAGCATCGTGAAAAAGAAAGAGCTTCCA 600
Db 541 AGTGGTCCCCAAGATGACCCCCACCCACGAGGAGCATCGTGAAAAAGAAAGAGCTTCCA 600
Qy 601 ACCAGCTCTTCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA 660
Db 601 ACCAGCTCTTCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCA 660
Qy 661 CAATCCCACTATCTTCGCAAGACCTTCTCTATATAAGAAAGTTCATTTTCAATTTGGAG 720
Db 661 CAATCCCACTATCTTCGCAAGACCTTCTCTATATAAGAAAGTTCATTTTCAATTTGGAG 720
Qy 721 AGGACACGCTGGATCC 736
Db 721 AGGACACGCTGGATCC 736

RESULT 2
US-10-075-105C-3
; Sequence 3, Application US/10075105C
; Publication No. US20050188432A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zhijian T
; APPLICANT: Gray, Dennis J
; TITLE OF INVENTION: Bi-Directional Dual Promoter Complex with Enhanced Promoter Activity
; FILE REFERENCE: 7270-72978
; CURRENT FILING DATE: 2002-02-13
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; TYPE: DNA
; ORGANISM: CaMV 35S
; FEATURE:
; OTHER INFORMATION:

US-10-075-105C-3
Query Match 81.2%; Score 597.4; DB 22; Length 1360;
Best Local Similarity 99.8%; Pred. No. 2.2e-191;
Matches 598; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 109 AGAAGCTTCTGCAAGTGGAGCTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTC 168
Db 762 ATAAGCTTCTGCAAGTGGAGCTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTC 821
Qy 169 CATTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAGAAAGAGGTCGACCTAC 228
Db 822 CATTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAGAAAGAGGTCGACCTAC 881
Qy 229 AAATGCCATCATTCGGATAAAGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGT 288
Db 882 AAATGCCATCATTCGGATAAAGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGT 941
Qy 289 CCAAAAGATGGACCCACCCACGAGGAGCATCGTGAAAAAGAAAGAGCTTCCAAACCAAG 348
Db 942 CCAAAAGATGGACCCACCCACGAGGAGCATCGTGAAAAAGAAAGAGCTTCCAAACCAAG 1001
Qy 349 TCTTCAAAGCAAGTGGATTGATGTGATTCAGTGAGACTTTTCAACAAAGGTAATATCG 408
Db 1002 TCTTCAAAGCAAGTGGATTGATGTGATTCAGTGAGACTTTTCAACAAAGGTAATATCG 1061
Qy 409 GGAACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAA 468
Db 1062 GGAACCTCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAA 1121
Qy 469 AAGGAAGTGGACACCTTCAAAATGCCATCATTCGGATAAAGAAAGGCTATCGTTCAAGAT 528
Db 1122 AAGGAAGTGGACACCTTCAAAATGCCATCATTCGGATAAAGAAAGGCTATCGTTCAAGAT 1181
Qy 529 GCCTCTCCGACAGTGGTCCCAAGATGGACCCCAAGAGGAGCATCGTGAAAAA 588
Db 1182 GCCTCTCCGACAGTGGTCCCAAGATGGACCCCAAGAGGAGCATCGTGAAAAA 1241
Qy 589 GAGAGCTTCCACACGCTTCAAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTA 648
Db 1242 GAAGAGCTTCCACACGCTTCAAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTA 1301
Qy 649 AGGGATGAGGCAACATCCCACTATCTTCGCAAGACCTTCTCTATATAAGAAAGTTC 707
Db 1302 AGGGATGAGGCAACATCCCACTATCTTCGCAAGACCTTCTCTATATAAGAAAGTTC 1360

RESULT 3
US-09-943-692-33
; Sequence 33, Application US/09943692
; Patent No. US20020152496A1
; GENERAL INFORMATION:
; APPLICANT: FISCHHOFF, DAVID A.
; APPLICANT: FUCHS, ROY L.
; APPLICANT: LAVRIK, PAUL B.
; APPLICANT: McPHERSON, SYLVIA A.
; APPLICANT: PERLAK, FREDERICK J.
; TITLE OF INVENTION: COLBOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
; FILE REFERENCE: MOBT:195--1
; CURRENT FILING DATE: 2001-08-31
; PRIOR FILING DATE: 1998-02-23
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 33
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Cauliflower Mosaic Viral Promoter (CaMV35S)
US-09-943-692-33

Query Match 75.3%; Score 554; DB 9; Length 661;
Best Local Similarity 94.5%; Pred. No. 8e-177;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
Qy 116 TCTCAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 175
Db 20 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 79
Qy 176 CAGCTATCTGTCACCTTCAATCAAAAGGACAGTAGAAGGAGGAGGTCGACCTTACAAATGCC 235
Db 80 CAGCTATCTGTCACCTTATTTGTAAGATAGTGAAGAGGAGGTCGTCCTTACAAATGCC 139
Qy 236 ATCAATTGCGATAAAGGAAAGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 295
Db 140 ATCAATTGCGATAAAGGAAAGGCTATCGTTGAAGATGCTCTGCCGACAGTGGTCCCAAAG 199
Qy 296 ATGGACCCCCACCCAGGAGGACATCGTGGAAAGAGAGGTCGTCACCAACCAAGCTTTCAA 355
Db 200 ATGGACCCCCACCCAGGAGGACATCGTGGAAAGAGAGGTCGTCACCAACCAAGCTTTCAA 259
Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db 260 AGCAAGTGGATTGATGTGATGTGTCGATGTGAGACTTTTCAACAAAGGGTAATATCGGA 319
Qy 412 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTCAATCAAAAGGACAGTAGAAG 471
Db 320 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTATTTGTAAGATAGTGGAAAG 379
Qy 472 GAAGTGGACCTACAAATGTCATTCGATGCGATTAAGGAAAGGTCATCGTTCAAGATGCC 531
Db 380 GAAGTGGCTCTTCAAAATGTCATTTGCGATTAAGGAAAGGTCATCGTTGAAGATGCC 439
Qy 532 TCTCCGACAGTGGTCCAAAGATGGACCCCAACCCAGAGGAGCATCGTGGAAAGAA 591
Db 440 TCTCCGACAGTGGTCCAAAGATGGACCCCAACCCAGAGGAGCATCGTGGAAAGAA 499
Qy 592 GACGTTCCAAACCAAGCTTTCAAGCAAGTGAATGTGATATCTCCACTGACGTAAGG 651
Db 500 GACGTTCCAAACCAAGCTTTCAAGCAAGTGAATGTGATATCTCCACTGACGTAAGG 559
Qy 652 GATGACGCAATCCCACTATCTTCCGACAGCCCTTCTCTATATAAGGAAATTCATTT 711
Db 560 GATGACGCAATCCCACTATCTTCCGACAGCCCTTCTCTATATAAGGAAATTCATTT 619
Qy 712 CATTTGGAGGACACGCTG 731
Db 620 CATTTGGAGGACACGCTG 639

RESULT 4
US-10-213-791-29
; Sequence 29, Application US/10213791
; Publication No. US20030106096A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/10/213,791
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/441,340
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/108,763
; PRIOR FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 2107
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; OTHER INFORMATION: cassette comprising plant operable promoter linked
; OTHER INFORMATION: to a leader, intron, a sequence encoding an AMPA

OTHER INFORMATION: acetyltransferase, and termination sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (26)..(590)
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (615)..(685)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (699)..(1148)
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1149)..(1426)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1427)..(1858)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (1869)..(2102)
; US-10-213-791-29

Query Match 75.3%; Score 554; DB 15; Length 2107;
Best Local Similarity 94.5%; Pred. No. 1.4e-176;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;
Qy 116 TCTCAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 175
Db 28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTTGCC 87
Qy 176 CAGCTATCTGTCACCTTCAATCAAAAGGACAGTAGAAGGAGGTCGACCTTACAAATGCC 235
Db 88 CAGCTATCTGTCACCTTTATTTGTAAGATAGTGGAAAGGAGGTCCTCTACAAATGCC 147
Qy 236 ATCAATTGCGATAAAGGAAAGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 295
Db 148 ATCAATTGCGATAAAGGAAAGGCTATCGTTGAAGATGCTCTGCCGACAGTGGTCCCAAAG 207
Qy 296 ATGGACCCCCACCCAGGAGGACATCGTGGAAAGAGAGGTCGTCACCAACCAAGCTTTCAA 355
Db 208 ATGGACCCCCACCCAGGAGGACATCGTGGAAAGAGAGGTCGTCACCAACCAAGCTTTCAA 267
Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
Db 268 AGCAAGTGGATTGATGTGATGTGTCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 327
Qy 412 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTCAATCAAAAGGACAGTAGAAG 471
Db 328 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTTATTTGTAAGATAGTGGAAAG 387
Qy 472 GAAGTGGACCTTACAAATCCCACTATTTGCGATAAAGGAAAGGTCATCGTTCAAGATGCC 531
Db 388 GAAGTGGCTCTTACAAATGCCATCATTTGCGATAAAGGAAAGGTCATCGTTGAAGATGCC 447
Qy 532 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCAGGAGGAGCATCGTGGAAAGAA 591
Db 448 TCTGCCGACAGTGGTCCCAAGATGGACCCCAACCCAGGAGGAGCATCGTGGAAAGAA 507
Qy 592 GACGTTCCCAACCAAGCTTTCAAGCAAGTGAATGTGATATCTCCACTGACGTAAGG 651
Db 508 GACGTTCCCAACCAAGCTTTCAAGCAAGTGAATGTGATATCTCCACTGACGTAAGG 567
Qy 652 GATGACGCAATCCCACTATCTTCCGACAGCCCTTCTCTATATAAGGAAATTCATTT 711
Db 568 GATGACGCAATCCCACTATCTTCCGACAGCCCTTCTCTATATAAGGAAATTCATTT 627
Qy 712 CATTTGGAGGACACGCTG 731
Db 628 CATTTGGAGGACACGCTG 647

RESULT 5
US-10-213-791-25
; Sequence 25, Application US/10213791

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; Publication No. US20030106096A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/10/213,791
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/441,340
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/108,763
; PRIOR FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 2122
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:expression
; OTHER INFORMATION: cassette comprising plant promoter linked to
; OTHER INFORMATION: sequence encoding AMPA acetyl transferase linked
; OTHER INFORMATION: to termination sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (6)..(620)
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (645)..(715)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (729)..(1178)
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1179)..(1406)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1407)..(1838)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (1849)..(2082)
; US-10-213-791-25

Query Match 75.3%; Score 554; DB 15; Length 2122;
Best Local Similarity 94.5%; Pred. No. 1.4e-176;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTGAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
Db 8 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 67

Qy 176 CAGCTATCTGCTCACTTTCATCAAAAGGACAGTAGAAAAGGAGGTGGCACCTACAAATGCC 235
Db 68 CAGCTATCTGCTCACTTTCATCAAAAGGACAGTAGAAAAGGAGGTGGCTCTACAAATGCC 127

Qy 236 ATCATTCGCGATAAAGGAAGGCTATCGTTCAAGATGCTCTCGCGACAGTGGTCCCAAAG 295
Db 128 ATCATTCGCGATAAAGGAAGGCTATCGTTCAAGATGCTCTCGCGACAGTGGTCCCAAAG 187

Qy 296 ATGACCCCCCACCACGAGGAGCATCGTGGAAAAGAACGTTCCAAACCACTCTTCAA 355
Db 188 ATGACCCCCCACCACGAGGAGCATCGTGGAAAAGAACGTTCCAAACCACTCTTCAA 247

Qy 356 AGCAAGTGGATTCATGTGAT- - - - -TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGA 411
Db 248 AGCAAGTGGATTCATGTGATGTGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGA 307

Qy 412 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCAATCAAAAGGACAGTAGAAAAG 471
Db 308 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTATTCGTAAGATAGTGGAAAAG 367

Qy 472 GAAGGTGGCACTTACAAATGCCATCATTCGCGATAAGGAAAGGCTATCGTTCAAGATGCC 531
Db 368 GAAGGTGGCTCTTACAAATGCCATCATTCGCGATAAGGAAAGGCTATCGTTCAAGATGCC 427

; Publication No. US20030106096A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/10/213,791
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/441,340
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/108,763
; PRIOR FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 2122
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:expression
; OTHER INFORMATION: cassette comprising plant promoter linked to
; OTHER INFORMATION: sequence encoding AMPA acetyl transferase linked
; OTHER INFORMATION: to termination sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (6)..(620)
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (645)..(715)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (729)..(1178)
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1179)..(1406)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1407)..(1838)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (1849)..(2082)
; US-10-213-791-25

Query Match 75.3%; Score 554; DB 15; Length 2436;
Best Local Similarity 94.5%; Pred. No. 1.5e-176;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTGAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 175
Db 28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTGCC 87

Qy 176 CAGCTATCTGCTCACTTTCATCAAAAGGACAGTAGAAAAGGAGGTGGCACCTACAAATGCC 235
Db 88 CAGCTATCTGCTCACTTTCATCAAAAGGAGTAGTAGTGGAAAAGGAGGTGGCTCTCAAAATGCC 147

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Qy 236 ATCATTCGATAAAGGAAAGCTATCGTTCAAGATGCTCTGCGCAGAGTGTCCTCCCAAG 295
Db 148 ATCATTCGATAAAGGAAAGCCATCGTTGAAGATGCTCTGCGCAGAGTGTCCTCCCAAG 207
Qy 296 ATGACACCCCAACCCAGAGGAGCTGCGGAAAGAGAGCTTCCCAACACGCTCTTCAA 355
Db 208 ATGACACCCCAACCCAGAGGAGCTGCGGAAAGAGAGCTTCCCAACACGCTCTTCAA 267
Qy 356 AGCAAGTGGAATGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGTAATATCGGA 411
Db 268 AGCAAGTGGAATGATGTGATGTGCGATGTCGATCTTCAACAAAGGTAATATCGGA 327
Qy 412 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGACAGTAGAGAAAG 471
Db 328 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 387
Qy 472 GAAGTGCGACCTACAAATGCATTCGATGCGATAAAGGAAGGCTATCGTTCAAGATGCC 531
Db 388 GAAGTGCGCTCTCAAAATGCATTCGATGCGATAAAGGAAGGCTATCGTTGAAGATGCC 447
Qy 532 TCTGCCGACAGTGTCCCAAGATGGACCCCAACCCAGAGGAGCATCGTGGAAAAAGAA 591
Db 448 TCTGCCGACAGTGTCCCAAGATGGACCCCAACCCAGAGGAGCATCGTGGAAAAAGAA 507
Qy 592 GACGTTCCAAACCAAGCTTTCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 651
Db 508 GACGTTCCAAACCAAGCTTTCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 567
Qy 652 GATGACGACAAATCCCACTATCTTCCGACAGCCCTTCTCTATATAAGGAAGTTCATTT 711
Db 568 GATGACGACAAATCCCACTATCTTCCGACAGCCCTTCTCTATATAAGGAAGTTCATTT 627
Qy 712 CATTTGGAGAGGACACGCTG 731
Db 628 CATTTGGAGAGGACACGCTG 647
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RESULT 7

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US-10-232-665-23
; Sequence 23, Application US/10232665
; Publication No. US20030115630A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/10/232,665
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 3469
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CaMV.35S
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (664)..(734)
; OTHER INFORMATION: L-Ta.hcbl
; FEATURE:
; NAME/KEY: intron
; LOCATION: (748)..(1238)
; OTHER INFORMATION: I-Os.Act1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1241)..(3199)
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; OTHER INFORMATION: Cry3Bb1 variant 11231mv2
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (3217)..(3450)
; OTHER INFORMATION: T-Ta.hsp17
; US-10-232-665-23
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Query Match 75.3%; Score 554; DB 15; Length 3469;

Best Local Similarity 94.5%; Pred. No. 1.9e-176;

Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

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Qy 116 TCTGCGAGTGAGACTTTTCAACAAAGGGTAATATATCGGAAACCTCTCGGATTCATTTGCC 175
Db 28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATATCGGAAACCTCTCGGATTCATTTGCC 87
Qy 176 CAGCTATCTCTCACTTCATCAAAAGGACAGTAGAAAAAGGAGGTGGCACCTACAAATGCC 235
Db 88 CAGCTATCTCTCACTTTATTGTGAAGATAGTGGAAAAGGAGGTGGCTCTACAAATGCC 147
Qy 236 ATCATTCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGCAGAGTGTCCTCCCAAG 295
Db 148 ATCATTCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGCAGAGTGTCCTCCCAAG 207
Qy 296 ATGACACCCCAACCCAGAGGAGCATCGTGGAAAAAGAGAGCTTCCCAACACGCTCTTCAA 355
Db 208 ATGACACCCCAACCCAGAGGAGCATCGTGGAAAAAGAGAGCTTCCCAACACGCTCTTCAA 267
Qy 356 AGCAAGTGGAATGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGTAATATCGGA 411
Db 268 AGCAAGTGGAATGATGTGATGTGCGATGTCGATCTTCAACAAAGGTAATATCGGA 327
Qy 412 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAGAAAG 471
Db 328 AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 387
Qy 472 GAAGTGCGACCTACAAATGCATTCGATGCGATAAAGGAAGGCTATCGTTCAAGATGCC 531
Db 388 GAAGTGCGCTCTCAAAATGCATTCGATGCGATAAAGGAAGGCTATCGTTGAAGATGCC 447
Qy 532 TCTGCCGACAGTGTCCCAAGATGGACCCCAACCCAGAGGAGCATCGTGGAAAAAGAA 591
Db 448 TCTGCCGACAGTGTCCCAAGATGGACCCCAACCCAGAGGAGCATCGTGGAAAAAGAA 507
Qy 592 GACGTTCCAAACCAAGCTTTCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 651
Db 508 GACGTTCCAAACCAAGCTTTCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 567
Qy 652 GATGACGACAAATCCCACTATCTTCCGACAGCCCTTCTCTATATAAGGAAGTTCATTT 711
Db 568 GATGACGACAAATCCCACTATCTTCCGACAGCCCTTCTCTATATAAGGAAGTTCATTT 627
Qy 712 CATTTGGAGAGGACACGCTG 731
Db 628 CATTTGGAGAGGACACGCTG 647
```

RESULT 8

```
US-10-232-665-15
; Sequence 15, Application US/10232665
; Publication No. US20030115630A1
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/10/232,665
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 3754
; TYPE: DNA
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: expression
OTHER INFORMATION: cassette

FEATURE:
NAME/KEY: promoter

LOCATION: (25)..(640)

OTHER INFORMATION: P-CaMV.35S

FEATURE:
NAME/KEY: intron

LOCATION: (669)..(1472)

OTHER INFORMATION: I-Zm.Hsp70

FEATURE:
NAME/KEY: CDS

LOCATION: (1490)..(3448)

OTHER INFORMATION: Cry3Bb1 variant v11231

FEATURE:
NAME/KEY: terminator

LOCATION: (3475)..(3730)

OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription

OTHER INFORMATION: termination and polyadenylation sequence

US-10-232-665-15

Query Match 75.3%; Score 554; DB 15; Length 3754;
Best Local Similarity 94.5%; Pred. No. 1.9e-176;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy	116	TCTGCAGTGAGACTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCGATGCC	175
Db	28	TCCGATGTGAGCTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCGATGCC	87
Qy	176	CAGCTATCTGTCACCTTCATCAAAAGGACAGTAGAAGAGGAGTGCGACCTACAAATGCC	235
Db	88	CAGCTATCTGTCACCTTTATTGTGAAGATAGTGGAAAGGAGTGCGCTCTACAAATGCC	147
Qy	236	ATCATTCGGATAAAGAAAGGCTATCGTTCAAGATGCTCTCGCGACAGTGGTCCCAAAAG	295
Db	148	ATCATTCGGATAAAGAAAGGCTATCGTTCAAGATGCTCTCGCGACAGTGGTCCCAAAAG	207
Qy	296	ATGACACCCACCCACAGAGAGCATCGTGGAAAGAAAGAGCTTCCAAACACGCTTTCAA	355
Db	208	ATGACACCCACCCACAGAGAGCATCGTGGAAAGAAAGAGCTTCCAAACACGCTTTCAA	267
Qy	356	AGCAAGTGGATTGATGTGAT- ---TGCAAGTGAGACTTTTCAACAAAGGTAATATCGGA	411
Db	268	AGCAAGTGGATTGATGTGATGCTGCGATGTGAGACTTTTCAACAAAGGTAATATCGGA	327
Qy	412	AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAG	471
Db	328	AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAG	387
Qy	472	GAAGTGGACCTACAAATGCCATCATTCGGATAAGAAAGGCTATCGTTCAAGATGCC	531
Db	388	GAAGTGGCTCCTACAAATGCCATCATTCGGATAAGAAAGGCTATCGTTCAAGATGCC	447
Qy	532	TCTGCCACAGTGTCTCCAAAGATGGACCCACCCACAGGAGCATCGTGGAAAGAAAG	591
Db	448	TCTGCCACAGTGTCTCCAAAGATGGACCCACCCACAGGAGCATCGTGGAAAGAAAG	507
Qy	592	GACGTTCCAAACCAAGCTTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG	651
Db	508	GACGTTCCAAACCAAGCTTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG	567
Qy	652	GATGACGCACAAATCCCACTATCTTCGCAAGACCCCTTCTATATAAGGAAGTTCATTT	711
Db	568	GATGACGCACAAATCCCACTATCTTCGCAAGACCCCTTCTATATAAGGAAGTTCATTT	627
Qy	712	CATTGGAGAGGACACGCTG 731	
Db	628	CATTGGAGAGGACACGCTG 647	

US-10-198-478-16
Sequence 16, Application US/10198478
Publication No. US20030188336A1
GENERAL INFORMATION:
APPLICANT: Corbin, David R.
TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotoxin
FILE REFERENCE: 38-21 (13547) B
CURRENT APPLICATION NUMBER: US/10/198,478
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 09/186,002
PRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 8349
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: completely synthesized
NAME/KEY: misc_feature
LOCATION: (1)..(8349)
OTHER INFORMATION:
US-10-198-478-16

Query Match 75.3%; Score 554; DB 16; Length 8349;
Best Local Similarity 94.5%; Pred. No. 2.9e-176;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy	116	TCTGCAGTGAGACTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCGATGCC	175
Db	1807	TCCGATGTGAGACTTTTCAACAAAGGTAATATCGGAAACCTCTCGGATTCGATGCC	1866
Qy	176	CAGCTATCTGTCACCTTCATCAAAAGGACAGTAGAAGAGGAGTGCGACCTACAAATGCC	235
Db	1867	CAGCTATCTGTCACCTTTATTGTGAAGATAGTGGAAAGGAGTGCGCTCTACAAATGCC	1926
Qy	236	ATCATTCGGATAAAGAAAGGCTATCGTTCAAGATGCTCTCGCGACAGTGGTCCCAAG	295
Db	1927	ATCATTCGGATAAAGAAAGGCTATCGTTCAAGATGCTCTCGCGACAGTGGTCCCAAG	1986
Qy	296	ATGACACCCACCCACAGAGAGCATCGTGGAAAGAAAGAGCTTCCAAACACGCTTTCAA	355
Db	1987	ATGACACCCACCCACAGAGAGCATCGTGGAAAGAAAGAGCTTCCAAACACGCTTTCAA	2046
Qy	356	AGCAAGTGGATTGATGTGAT- ---TGCAAGTGAGACTTTTCAACAAAGGTAATATCGGA	411
Db	2047	AGCAAGTGGATTGATGTGATGCTGCGATGTGAGACTTTTCAACAAAGGTAATATCGGA	2106
Qy	412	AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAG	471
Db	2107	AACCTCTCGGATTCATTCGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAG	2166
Qy	472	GAAGTGGACACCTACAAATGCCATCATTCGGATAAGAAAGGCTATCGTTCAAGATGCC	531
Db	2167	GAAGTGGCTCTCTACAAATGCCATCATTCGGATAAGAAAGGCTATCGTTGAAGATGCC	2226
Qy	532	TCTGCCACAGTGTCTCCAAAGATGGACCCACCCACAGGAGCATCTGTTGGAAAGAAAG	591
Db	2227	TCTGCCACAGTGTCTCCAAAGATGGACCCACCCACAGGAGCATCTGTTGGAAAGAAAG	2286
Qy	592	GAGGTTCCAAACCAAGCTTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG	651
Db	2287	GAGGTTCCAAACCAAGCTTTCAAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG	2346
Qy	652	GATGACGCACAAATCCCACTATCTTCGCAAGACCCCTTCTATATAAGGAAGTTCATTT	711
Db	2347	GATGACGCACAAATCCCACTATCTTCGCAAGACCCCTTCTATATAAGGAAGTTCATTT	2406
Qy	712	CATTGGAGAGGACACGCTG 731	
Db	2407	CATTGGAGAGGACACGCTG 2426	


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RESULT 10
US-10-378-810-2/c
; Sequence 2, Application US/10378810
; Publication No. US20030213009A1
; GENERAL INFORMATION:
; APPLICANT: Ruben-Wilson, Beth
; APPLICANT: Smith, Kelley A
; TITLE OF INVENTION: PROMOTER AND INTRON FROM MAIZE ACTIN DEPOLYMERIZING
; FILE REFERENCE: 58695
; CURRENT APPLICATION NUMBER: US/10/378,810
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 60/167,111
; PRIOR FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 5796
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pDAB305
US-10-378-810-2

Query Match          74.9%; Score 551.4; DB 17; Length 5796;
Best Local Similarity 93.2%; Pred. No. 1.8e-175;
Matches 588; Conservative 0; Mismatches 41; Indels 2; Gaps 1;

Qy 105 CTGCAGAGCTTCTGCAAGTGGAGACTTTTCAACAAGGGTAAATATCGGGAAACCTCTCGG 164
Db 3550 CTGCAGATCTGCATGGGTGGAGACTTTTCAACAAGGGTAAATATCGGGAAACCTCTCGG 3491

Qy 165 ATTCATGCCCCAGCTATCTGCTACTTCATCAAAAGGACAGTACAAAAGGAGGTGGCAC 224
Db 3490 ATTCATGCCCCAGCTATCTGCTACTTTATTTGTGAAGATAGTGGAAAAGGAGGTGGCTC 3431

Qy 225 CTACAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGGACAG 284
Db 3430 CTACAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTTGAAGATGCTCTGCGGACAG 3371

Qy 285 TGGTCCAAAGATGGAGCCCCCACCACGAGGAGCATCGTGGAAAAAGAACGCTTCCAAC 344
Db 3370 TGGTCCAAAGATGGAGCCCCCACCACGAGGAGCATCGTGGAAAAAGAACGCTTCCAAC 3311

Qy 345 CACGTCTTCAAGCAAGTGGATTGATGTGAT--TGCAGTGAAGCTTTTCAACAAGGTA 402
Db 3310 CACGTCTTCAAGCAAGTGGATTGATGTGATCATCGATGGAGACTTTTCAACAAGGTA 3251

Qy 403 ATATCGGAAACCTCTCGGATTCATTGGCCAGCTATCTGCTACTTCATCAAAAGGACA 462
Db 3250 ATATCGGAAACCTCTCGGATTCATTGGCCAGCTATCTGCTACTTTATTTGTGAAGATA 3191

Qy 463 GTAGAAAAGGAGGTGGCACCCTACAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTT 522
Db 3190 GTGAAAAGGAGGAGTGGCTCTCTACAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTT 3131

Qy 523 CAAGATGCTCTGCGACAGTGGTCCCAAGATGAGCCCCCACCACGAGGAGCATCGTG 582
Db 3130 GAAGATGCTCTGCGACAGTGGTCCCAAGATGAGCCCCCACCACGAGGAGCATCGTG 3071

Qy 583 GAAAAGAGGAGCTTCCAAACCAAGCTTTCAAGCAAGTGGATTGATGTGATATCTCCACT 642
Db 3070 GAAAAGAGGAGCTTCCAAACCAAGCTTTCAAGCAAGTGGATTGATGTGATATCTCCACT 3011

Qy 643 GACGTAAAGGATGACGCAAAATCCCACTATCTTTGCAAGACCCCTTCTCTATATAAGGA 702
Db 3010 GACGTAAAGGATGACGCAAAATCCCACTATCTTTGCAAGACCCCTTCTCTATATAAGGA 2951

Qy 703 AGTTCAATTTCTTTGGAGAGGACAGCTGGA 733
Db 2950 AGTTCAATTTCTTTGGAGAGGACAGCTGGA 2920
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RESULT 11
US-10-759-602-26
; Sequence 26, Application US/10759602
; Publication No. US20040143868A1
; GENERAL INFORMATION:
; APPLICANT: Ainley, Michael
; APPLICANT: Armstrong, Katherine
; Belmar, Scott
; Folkerts, Otto
; Hopkins, Nicole
; Menke, Michael A.
; Paredy, Dayakar
; Petolino, Joseph F.
; Smith, Kelley
; Woosley, Aaron
; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DowAgroSciences LLC
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/759,602
; FILING DATE: 16-Jan-2004
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317 337 5110
; TELEFAX: 317 337 4847
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5897 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-759-602-26
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Query Match          74.9%; Score 551.4; DB 19; Length 5897;
Best Local Similarity 93.2%; Pred. No. 1.9e-175;
Matches 588; Conservative 0; Mismatches 41; Indels 2; Gaps 1;

Qy 105 CTGCAGAGCTTCTGCAAGTGGAGACTTTTCAACAAGGGTAAATATCGGGAAACCTCTCGG 164
Db 12 CTGCAGATCTGCATGGGTGGAGACTTTTCAACAAGGGTAAATATCGGGAAACCTCTCGG 71

Qy 165 ATTCATGCCCCAGCTATCTGCTACTTCATCAAAAGGACAGTACAAAAGGAGGTGGCAC 224
Db 72 ATTCATGCCCCAGCTATCTGCTACTTTATTTGTGAAGATAGTGGAAAAGGAGGTGGCTC 131

Qy 225 CTACAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTTCAAGATGCTCTGCGGACAG 284
Db 132 CTACAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTTGAAGATGCTCTGCGGACAG 191

Qy 285 TGGTCCAAAGATGGAGCCCCCACCACGAGGAGCATCGTGGAAAAAGAACGCTTCCAAC 344
Db 192 TGGTCCAAAGATGGAGCCCCCACCACGAGGAGCATCGTGGAAAAAGAACGCTTCCAAC 251

Qy 345 CACGTCTTCAAGCAAGTGGATTGATGTGAT--TGCAGTGAAGCTTTTCAACAAGGTA 402
Db 252 CACGTCTTCAAGCAAGTGGATTGATGTGATCATCGATGGAGACTTTTCAACAAGGTA 311
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QY 403 ATATCGGAAACCTCTCGGATTCATTGCCAGCTATCTGTCACTTCATCAAAAGGACA 462
| | | | |
Db 312 ATATCGGAAACCTCTCGGATTCATTGCCAGCTATCTGTCACTTCATCAAAAGGACA 371
| | | | |
QY 463 GTAGAAAAGGAAGTGGCAGCTTCAAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTT 522
| | | | |
Db 372 GTGAAAAGGAAGTGGCTCTCTACAAATGCCATCATTTGCGATAAAGGAAAGGCCATCGTT 431
| | | | |
QY 523 CAGATCGCTCTGCGGACAGTGGTCCCAAAGATGGACCCCAACCCACGAGGAGCATCGTG 582
| | | | |
Db 432 GAAGATCGCTCTGCGGACAGTGGTCCCAAAGATGGACCCCAACCCACGAGGAGCATCGTG 491
| | | | |
QY 583 GAAAAGAAGACGTTCCAAACCACTCTTCAAAAGCAAGTGGATGTGATATCTCCACT 642
| | | | |
Db 492 GAAAAGAAGACGTTCCAAACCACTCTTCAAAAGCAAGTGGATGTGATATCTCCACT 551
| | | | |
QY 643 GACGTAAGGATGACGACCAATCCCACTATCTTTCGCAAGACCTTCCCTCTATATAAGGA 702
| | | | |
Db 552 GACGTAAGGATGACGACCAATCCCACTATCTTTCGCAAGACCTTCCCTCTATATAAGGA 611
| | | | |
QY 703 AGTTCATTTTCATTGGAGAGGACACGCTGGA 733
| | | | |
Db 612 AGTTCATTTTCATTGGAGAGGACACGCTGGA 642
| | | | |

RESULT 12
US-10-759-602-19
; Sequence 19, Application US/10759602
; Publication No. US20040143868A1
; GENERAL INFORMATION:
; APPLICANT: Ainley, Michael
; Armstrong, Katherine
; Belmar, Scott
; Folkerts, Otto
; Hopkins, Nicole
; Menke, Michael A.
; Paredy, Davakar
; Petolino, Joseph P.
; Smith, Kelley
; Woosley, Aaron
; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DowAgroSciences LLC
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 16-Jan-2004
; APPLICATION NUMBER: US/10/759,602
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317 337 5110
; TELEFAX: 317 337 4847
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-759-602-19

Query Match 74.8%; Score 550.4; DB 19; Length 9335;
Best Local Similarity 93.2%; Pred. No. 5.1e-175;
Matches 587; Conservative 0; Mismatches 41; Indels 2; Gaps 1;
QY 106 TGCAGAAAGCTTCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCTCTCGGA 165
| | | | |
Db 4852 TGCAGATTCGATGGGTGGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCTCTCGGA 4911
| | | | |
QY 166 TTCCATTTGCCAGCTATCTGTCTCACTTCAATCAAAAGGACAGTAGAAAAGGAGGTGGCACC 225
| | | | |
Db 4912 TTCCATTTGCCAGCTATCTGTCTCACTTATTTGTGAAGATAGTGAAAAGGAGGTGGCTCC 4971
| | | | |
QY 226 TCAAAATGCCATCATTTGCGATAAAGGAGGCTATCGTTCAAGATCGCTCTGCGGACAGT 285
| | | | |
Db 4972 TCAAAATGCCATCATTTGCGATAAAGGAGGCTATCGTTGAAGATGCCTCTGCGGACAGT 5031
| | | | |
QY 286 GGTCCCAAAGATGAGACCCCAACCCACGAGGAGCATCGTGGAAAAGAAAGACGTTTCCAACC 345
| | | | |
Db 5032 GGTCCCAAAGATGAGACCCCAACCCACGAGGAGCATCGTGGAAAAGAAAGACGTTTCCAACC 5091
| | | | |
QY 346 ACCTCTTCAAAAGCAAGTGGATGTGTAT--TGCAGTGAGACTTTTCAACAAAGGGTAA 403
| | | | |
Db 5092 ACCTCTTCAAAAGCAAGTGGATGTGTATCATCGATGGAGACTTTTCAACAAAGGGTAA 5151
| | | | |
QY 404 TATCGGGAACCTCTCTCGGATTCATTGCCAGCTATCTGTCACTTCATCAAAAGGACAG 463
| | | | |
Db 5152 TATCGGGAACCTCTCTCGGATTCATTGCCAGCTATCTGTCACTTTATTTGGAAGATAG 5211
| | | | |
QY 464 TAGAAAAGGAAGTGGCAGCTTCAAAATGCCATCATTTGCGATAAAGGAAAGGCTATCGTTC 523
| | | | |
Db 5212 TGGAAAAGGAAGTGGCTCTCTCAAAATGCCATCATTTGCGATAAAGGAAAGGCCATCGTTG 5271
| | | | |
QY 524 AGATGCTCTTGCAGACAGTGGTCCCAAAGATGAGACCCCAACCCACGAGAGAGCATCGTGG 583
| | | | |
Db 5272 AGATGCTCTTGCAGACAGTGGTCCCAAAGATGAGACCCCAACCCACGAGAGAGCATCGTGG 5331
| | | | |
QY 584 AAAAAAGAACGTTTCCAAACCACTCTTCAAAAGCAAGTGGATTCATGTGATATCTCCACTG 643
| | | | |
Db 5332 AAAAAAGAACGTTTCCAAACCACTCTTCAAAAGCAAGTGGATTCATGTGATATCTCCACTG 5391
| | | | |
QY 644 ACCTAAGGATGACGACCAATCCCACTATCTTTCGCAAGACCTTCTCTATATAAGGAA 703
| | | | |
Db 5392 ACCTAAGGATGACGACCAATCCCACTATCTTTCGCAAGACCTTCTCTATATAAGGAA 5451
| | | | |
QY 704 GTTCATTTTCATTGGAGAGGACACGCTGGA 733
| | | | |
Db 5452 GTTCATTTTCATTGGAGAGGACACGCTGGA 5481
| | | | |
RESULT 13
US-10-198-478-14
; Sequence 14, Application US/10198478
; Publication No. US20030188336A1
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotoxin
; FILE REFERENCE: 38-21 (13547) B
; CURRENT APPLICATION NUMBER: US/10/198,478
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/186, 002
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 10249
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: completely synthesized
; FEATURE:
; NAME/KEY: misc_feature

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; LOCATION: (1)..(10249)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3597)..(3670)
; OTHER INFORMATION: "n" = g, a, c, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4292)..(4344)
; OTHER INFORMATION: "n" = g, a, c, or t
US-10-198-478-14

Query Match      74.7%; Score 550; DB 16; Length 10249;
Best Local Similarity 94.5%; Pred. No. 7.3e-175;
Matches 582; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

Qy 116 TCTCAGTGAGACTTTTCAACAAAGGGTAAATATCGGAAACCTCTCGGATTCATTTGCC 175
Db |||
Qy 19 TCCGATGTGAGACTTTTCAACAAAGGGTAAATATCGGAAACCTCTCGGATTCATTTGCC 78
Db |||
Qy 176 CAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAGAAAGGAGGTGGACCTTACAAATGCC 235
Db |||
Qy 79 CAGCTATCTGTCACTTATTGTGAAGATAGTGGAAAGGAGGTGGCTCTCTACAAATGCC 138
Qy 236 ATCATTTGGGATAAAGGAAAGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAG 295
Db |||
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Qy 296 ATGACACCCCAACCCAGGAGGACATCGTGGAAAGGAGGCTTCCAAACACGCTTTCAA 355
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Qy 356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAAATATCGGGA 411
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Qy 319 AACCTCTCGGATTCATTTGCCAGGCTATCGTCACTTATCAAAAGGAGTAGTGGAAAG 378
Qy 472 GAAGGTGGACCTACAAATGCCATTCATTTGGGATAAAGGAGGCTATCGTTCAAGATGCC 531
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Db |||
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Qy 592 GACGTTCAACACCGTCTTCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 651
Db |||
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Db |||
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RESULT 14

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US-10-198-478-15
; Sequence 15, Application US/10198478
; Publication No. US20030188336A1
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotoxin
; FILE REFERENCE: 38-21 (13547) B
; CURRENT APPLICATION NUMBER: US/10/198,478
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/186, 002
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RESULT 15

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; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
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; OTHER INFORMATION: completely synthesized
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; LOCATION: (1)..(10312)
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3660)..(3773)
; OTHER INFORMATION: "n" = g, a, c, or t
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; LOCATION: (4355)..(4407)
; OTHER INFORMATION: "n" = g, a, c, or t
US-10-198-478-15

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Best Local Similarity 94.5%; Pred. No. 7.3e-175;
Matches 582; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

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Db |||
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Qy 499 GACGTTCAACACCGTCTTCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 558
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Db |||
Qy 559 GATCAGCACAAATCCCACTATCTTCCAGACCCCTTCTCTATATAGGAAGTTCAATTT 618
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US-10-198-478-13
; Sequence 13, Application US/10198478
; Publication No. US20030188336A1
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotox
; FILE REFERENCE: 38-21 (13547) B
; CURRENT APPLICATION NUMBER: US/10/198,478
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 05/186, 002
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
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; OTHER INFORMATION: completely synthesized
; FEATURE:
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; OTHER INFORMATION:
; FEATURE:
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; OTHER INFORMATION: "n" = g, a, c, or t
US-10-198-478-13

Query Match 74.7%; Score 550; DB 16; Length 10339;
Best Local Similarity 94.5%; Pred. No. 7.3e-175;
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QY 412 AACCTCTCGGATTCATTTGCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAG 471
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QY 532 TCTGCCGACAGTGGTCCCAAGATGGACCCACCCACGAGGAGCATCGTGGAAAAGAA 591
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QY 592 GACGTTCCAAACCGCTTTCAAAGCAAGTGGATGTGATATCTCCACTGACGTAAGG 651
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QY 652 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTATATATAAGGAAGTTCATTT 711
DB 559 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTATATATAAGGAAGTTCATTT 618
QY 712 CATTTGGAGAGGACAC 727
DB 619 CATTTGGAGAGGACAC 634

Search completed: October 11, 2005, 15:38:12
Job time : 722 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 14:58:28 ; Search time 3213 Seconds
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Title: US-10-075-105C-1

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 segs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb_est1:*

2: gb_est2:*

3: gb_hc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	546.6	74.3	702	7	C0472768
3	546.6	74.3	755	7	CK438332
4	546.6	74.3	803	7	C0472761
5	544.6	74.0	713	7	CK437984
6	544.6	74.0	741	7	CK438362
7	537.2	73.0	655	7	CK437920
8	535.2	72.7	736	7	CK438485
9	533.2	72.4	698	7	CK438348
10	480.8	65.3	610	7	C0481168
11	351.8	47.8	839	8	AQ362115
12	341	46.3	654	9	CG206846
13	334.2	45.4	496	9	CG730119
14	332.6	45.2	467	8	B2591291
15	332.6	45.2	469	9	CG804983
16	332.6	45.2	490	8	B2586494
17	332.6	45.2	490	8	B2588196
18	332.6	45.2	524	8	B2586946
19	332.6	45.2	527	9	CG709568
20	332.6	45.2	528	9	CG805017
21	332.6	45.2	534	8	B2586497
22	332.6	45.2	534	8	B2586805
23	332.6	45.2	539	8	B2591222
24	332.6	45.2	543	8	B2587727

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c	26	332.6	45.2	549	8	BZ583905
c	27	332.6	45.2	570	8	BZ586953
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Picea glauca cDNA clone GQ0085_M18 5', mRNA sequence.
ACCESSION CK438483
VERSION CK438483.1 GI:40769778
KEYWORDS EST.
SOURCE Picea glauca (white spruce)
ORGANISM Picea glauca
REFERENCE 1 (bases 1 to 698)
AUTHORS Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A., Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J., Siddiqui,A., Holt,R., Marra,M. and Mackay,J.
Arborea EST sequencing in Picea glauca (white spruce)
Unpublished (2004)
COMMENT Contact: John Mackay
Centre de Recherche en Biologie Forestiere
Universite Laval
Pavillon Charles-Eugene Marchand, Quebec, Canada G1K 7P4
Fax: 418 656 7493
Email: jmackay@rsvs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN id Identifier: MN5174605 Clone ID:
GQ0085 M18 Clones available through: John Mackay, Ph. D. Professeur
adjoint -Assistant professeur EMAIL: jmackay@rsvs.ulaval.ca Centre
de Recherche en Biologie Forestiere (Forest Biology Research
Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
Plate: 5 row: 18 column: M
Seq primer: M13 Reverse Primer.
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from the midpoint of the main stem"
/dev_stage="Vascular cambium, secondary phloem, and bark
from trees harvested 1 and 7 days after girdling
treatment"
/lab_host="E. coli DH10B cells"

FEATURES

source
Location/Qualifiers
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of trees girdled by removing a ring of bark ca. 1 cm wide
from the midpoint of the main stem"
/dev_stage="Vascular cambium, secondary phloem, and bark
from trees harvested 1 and 7 days after girdling
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/clone_lib="GQ008: Cambium, phloem and bark of girdled saplings"
/note="Organ: Main stem of 4 year old saplings, approximately 60 cm tall; Vector: pBluescript II SK (+) XR; Site.1: Eco-R1; Site.2: Xho-I; Tissues were pooled from above and below the girdle. cDNA was prepared from 5 mg of poly A+ selected RNA and was directionally ligated into the pBluescript II SK (+) XR vector (Stratagene), transformed by electroporation into DH10B cells (in vitrogen) for propagation"

	Query Match	74.3%;	Score 546.6;	DB 7;	Length 698;
	Best Local Similarity	94.7%;	Pred. No. 1.8e-160;		
	Matches 577;	Conservative 0;	Mismatches 29;	Indels 3;	Gaps 1;
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Dd	124	TGGGATAAAGGAAGGCGCATCGTTGAAGATGCCCTCTCCGACAGCTGTGCCAAGATGGA	183		
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Qy	418	CTCGGATTCCATTGCCACGCTATCTGTCACTTCATCAAAGGACAGTAGAAAAGGAAGGT	477		
Dd	304	CTCGGATTCCATTGCCACGCTATCTGTCACTTTATTTGTGAAGATAGTGGAAAAGGAAGGT	363		
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LOCUS
DEFINITION
P0081.BR.1 K09 GQ008: Cambium, phloem and bark of girdled saplings
Picea glauca cDNA clone GQ0081.BR_K09 5', mRNA sequence.
ACCESSION
CO472768
VERSION
CO472768.1 GI:50141325
KEYWORDS
EST.
SOURCE
Picea glauca (white spruce)
ORGANISM
Picea glauca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.

REFERENCE
AUTHORS

TITLE	JOURNAL	COMMENT
1. The Role of the Teacher in the Classroom	Journal of Educational Research	1980, Vol. 83, No. 1, pp. 1-10
2. The Impact of Technology on Education	Journal of Educational Technology	1985, Vol. 10, No. 2, pp. 1-15
3. The Importance of Parental Involvement	Journal of Educational Psychology	1990, Vol. 82, No. 3, pp. 1-12
4. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	1995, Vol. 98, No. 4, pp. 1-18
5. The Role of the School in the Community	Journal of Educational Research	2000, Vol. 103, No. 5, pp. 1-20
6. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2005, Vol. 108, No. 6, pp. 1-25
7. The Role of the Teacher in the 21st Century	Journal of Educational Research	2010, Vol. 113, No. 7, pp. 1-30
8. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2015, Vol. 118, No. 8, pp. 1-35
9. The Role of the Teacher in the 21st Century	Journal of Educational Research	2020, Vol. 123, No. 9, pp. 1-40
10. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	2025, Vol. 128, No. 10, pp. 1-45

1 (bases 1 to 702)
Morency, M.-J., Cooke, J., Pavy, N., Parsons, L., Paule, C., Seguin, A.,
Retzel, E., Butterfield, Y., Barber, S., Yang, G., Stott, J.,
Siddiqui, A., Holt, R., Marra, M. and Mackay, J.
Arabore EST sequencing in *Picea glauca* (white spruce)
Unpublished (2004)
Contact: John Mackay
Centre de Recherche en Biologie Forestiere
Universite Laval
Pavillon Charles-Eugene Marchand, Quebec, Canada G1K 7P4
Fax: 418 656 7493
Email: jmackay@svs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN id Identifier: MN5197113 Clone ID:
GQ0081.BK.09 Clones available through: John Mackay, Ph. D.
Professeur adjoint -Assistant professor EMAIL:
jmackay@svs.ulaval.ca Centre de Recherche en Biologie Forestiere
(Forest Biology Research Center) Universite Laval Quebec, Quebec
Canada G1K 7P4

Plate: 1.BR row: 09 column: K
Seq primer: M13 Reverse Primer.

FEATURES source

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Location/Qualifiers
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/clone="GQ0081.BR K09"
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of trees girdled by removing a ring of bark ca. 1 cm wide
from the midpoint of the main stem"
/dev stages="Vascular cambium, secondary phloem, and bark
from trees harvested 1 and 7 days after girdling
treatment"
/lab host="E. coli DH10B cells"
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saplings"
/notes="Organ: Main stem of 4 year old saplings,
approximately 60 cm tall; Vector: pBluescript II SK (+)
XR; Site 1: Eco-R1; Site 2: Xho-I; Tissues were pooled
from above and below the girdle. cDNA was prepared from 5
mg of poly A+ selected RNA and was directionally ligated
into the pBluescript II SK (+) XR vector (Stratagene),
transformed by electroporation into DH10B cells (In
vitrogen) for propagation"

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ORIGIN

Query Match	74.3%;	Score 546.6;	DB 7;	Length 702;
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Matches 577;	Conservative 0;	Mismatches 29;	Indels 3;	Gaps 1;
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RESULT 3
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 LOCUS
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 Picea glauca cDNA clone GQ0083_H02 5', mRNA sequence.
 CK438332
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Picea glauca (white spruce)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
 1 (bases 1 to 755)
 Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A.,
 Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J.,
 Siddiqui A., Holt,R., Marra,M. and Mackay,J.
 Aborea EST sequencing in Picea glauca (white spruce)
 Unpublished (2004)
 Contact: John Mackay
 Centre de Recherche en Biologie Forestiere
 Universite Laval
 Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4
 Fax: 418 656 7493
 Email: jmackay@rsvs.ulaval.ca
 Center for Computational Genomics and Bioinformatics (CCGB),
 University of Minnesota, MN id Identifier: MN5173701 Clone ID:
 GQ0083_H02 Clones available through: John Mackay, Ph. D. Professeur
 adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
 de Recherche en Biologie Forestiere (Forest Biology Research
 Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
 Plate: 3 row: 02 column: H
 Seq primer: M13 Reverse Primer.
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 of trees girdled by removing a ring of bark ca. 1 cm wide
 from the midpoint of the main stem"
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 from trees harvested 1 and 7 days after girdling
 treatment"
 /lab_host="E. coli DH10B cells"
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 saplings"

FEATURES

source

RESULT 4
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 DEFINITION GQ0081_BR_1.G07 GQ008: Cambium, phloem and bark of girdled saplings
 Picea glauca cDNA clone GQ0081_BR_G07 5', mRNA sequence.
 CO472761
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Picea glauca (white spruce)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
 1 (bases 1 to 803)
 Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A.,

/note="Organ: Main stem of 4 year old saplings,
 approximately 60 cm tall; Vector: pBluescript II SK (+)
 XR; Site 1: Eco-RI; Site 2: Xho-I; Tissues were pooled
 from above and below the_girdle. cDNA was prepared from 5
 mg of poly A+ selected RNA and was directionally ligated
 into the pBluescript II SK (+) XR vector (Stratagene),
 transformed by electroporation into DH10B cells (in
 vitrogen) for propagation"

ORIGIN

Query Match 74.3%; Score 546.6; DB 7; Length 755;
 Best Local Similarity 94.7%; Pred. No. 1.9e-160;
 Matches 577; Conservative 0; Mismatches 29; Indels 3; Gaps 1;
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 Qy 361 GTGGATTGATGTGATTG---CAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTC 417
 Db 272 GTGGATTGATGTGATTGTCGATTCGATTTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTC 331
 Qy 418 CTGGATTTCATTCGCCAGCTATCTGTCACTTCATCAAAGGACAGTAGAAAAGGAAGGT 477
 Db 332 CTGGATTTCATTCGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGT 391
 Qy 478 GGCACTTACAAATGCCATCATTTGGGATAAAGGAAGGCTATCGTTCAAGATGCTCTGCC 537
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 Db 452 GACAGTGGTCCCAAGATGGACCCACCCACGAGGAGCATCGTGGAAAAGGAAGAGCGTT 511
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 Db 512 CCAACCACTCTTCAAGCAAGTGGATGATGCTATATCTCCACTGACGTAAAGGATGAC 571
 Qy 658 GCACAATCCCACTATCTTCCCAAGACCTTCTCTATATAAGGAAGTTCATTTCATTGG 717
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 Qy 718 GAGAGGACA 726
 Db 632 GAGAGGAGA 640

Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J., Siddiqui,A., Holt,R., Marra,M. and Mackay,J. Arborea EST sequencing in Picea glauca (white spruce) Unpublished (2004) Contact: John Mackay Centre de Recherche en Biologie Forestiere Universite Laval Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4 Fax: 418 656 7493 Email: jmackay@rsvs.ulaval.ca Center for Computational Genomics and Bioinformatics (CCGB) University of Minnesota, MN id Identifier: MN5198052 Clone ID: GQ0081.BR G07 Clones available through: John Mackay, Ph. D. Professeur adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre de Recherche en Biologie Forestiere (Forest Biology Research Center) Universite Laval Quebec, Quebec CANADA G1K 7P4 Plate: 1.BR row: 07 column: G Seq primer: M13 Reverse Primer. Location/Qualifiers 1..803 /organism="Picea glauca" /mol_type="mRNA" /strain="pg-653" /db_xref="taxon:3330" /clone="GQ0081.BR G07" /sex="Hermaphrodite" /tissue_type="Vascular cambium, secondary phloem and bark of trees girdled by removing a ring of bark ca. 1 cm wide from the midpoint of the main stem" /dev_stages="Vascular cambium, secondary phloem, and bark from trees harvested 1 and 7 days after girdling treatment" /lab_hosts="E. coli DH10B cells" /clone_lib="GQ008: Cambium, phloem and bark of girdled saplings"		713 bp mRNA linear EST 08-JAN-2004 GQ0081.BR_K09 GQ008: Cambium, phloem and bark of girdled saplings Picea glauca cDNA clone GQ0081_K09 5', mRNA sequence. CK437984 CK437984.1 GI:40768543 EST. Picea glauca (white spruce) Picea glauca Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea. 1 (bases 1 to 713) Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A., Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J., Siddiqui,A., Holt,R., Marra,M. and Mackay,J. Arborea EST sequencing in Picea glauca (white spruce) Unpublished (2004) Contact: John Mackay Centre de Recherche en Biologie Forestiere Universite Laval Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4 Fax: 418 656 7493 Email: jmackay@rsvs.ulaval.ca Center for Computational Genomics and Bioinformatics (CCGB), University of Minnesota, MN id Identifier: MN5171860 Clone ID: GQ0081_K09 Clones available through: John Mackay, Ph. D. Professeur adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre de Recherche en Biologie Forestiere (Forest Biology Research Center) Universite Laval Quebec, Quebec CANADA G1K 7P4 Plate: 1 row: 09 column: K Seq primer: M13 Reverse Primer. Location/Qualifiers 1..713 /organism="Picea glauca" /mol_type="mRNA" /strain="pg-653" /db_xref="taxon:3330" /clone="GQ0081_K09" /sex="Hermaphrodite" /tissue_type="Vascular cambium, secondary phloem and bark of trees girdled by removing a ring of bark ca. 1 cm wide from the midpoint of the main stem" /dev_stages="Vascular cambium, secondary phloem, and bark from trees harvested 1 and 7 days after girdling treatment" /lab_hosts="E. coli DH10B cells" /clone_lib="GQ008: Cambium, phloem and bark of girdled saplings"	
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Db	451	GACAGTGGTCCCAAGATGGACCCCAACGAGGAGCATCGTGAAGAAAGAGCGTT	510
QY	598	CCAACCACTCTTCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAAGGATGAC	657
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QY	658	GCACAATCCCACTATCTTTCGAAGACCTTCTCTATATAAGGAAGTTCATTTTCATTTG	717
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QY	718	GAGAGGACA	726
Db	631	GAGAGGAGA	639
RESULT 5			
CK437984			
LOCUS			
DEFINITION			
Picea glauca (white spruce)			
Picea glauca			
CK437984			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
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JOURNAL			
COMMENT			
FEATURES			
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of trees girdled by removing a ring of bark ca. 1 cm wide			
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from trees harvested 1 and 7 days after girdling			
treatment"			
/lab_hosts="E. coli DH10B cells"			
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saplings"			
ORIGIN			
Query Match 74.3%; Score 546.6; DB 7; Length 803;			
Best Local Similarity 94.7%; Pred. No. 1.9e-160;			
Matches 577; Conservative 0; Mismatches 29; Indels 3; Gaps 1;			
QY	121	AGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCGATGCCCGAGCT	180
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QY	241	TGGATAAAGAAAGGCTATCGTTTCAAGATGCCTCTGCCGACAGTGGTCCCAAGATGGA	300
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QY	418	CTCGATTTCATTCGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAAGGAGGT	477
Db	331	CTCGATTTCATTCGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAAGGAGGT	390

XR; Site_1: Eco-RI; Site_2: Xho-I; Tissues were pooled from above and below the girdle. cDNA was prepared from 5 mg of poly A+ selected RNA and was directionally ligated into the pBluescript II SK (+) XR vector (Stratagene), transformed by electroporation into DH10B cells (in vitrogen) for propagation"

ORIGIN

Query Match	74.0%	Score 544.6	DB 7	Length 713	
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QY	418	CTCGGATTTCATTGGCCAGCTATCTGTCACTTTCATCAAAAAGGACAGTAGAAAAAGGAAGGT	477		
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QY	478	GGCACTTACAAATGCCATCATTTGGGATAAAGGAAGGCTATCTGTTCAAGATGCCTCTGCC	537		
DB	364	GGCTCTTACAAATGCCATCATTTGGGATAAAGGAAGGCCATCTGTTGAAGATGCCTCTGCC	423		
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QY	598	CCAAACACAGTCTTCAAAGCAAGTGGATTGATGTGATATCTTCCACTGACGTAAGGGATGAC	657		
DB	484	CCAAACACAGTCTTCAAAGCAAGTGGATTGATGTGATATCTTCCACTGACGTAAGGGATGAC	543		
QY	658	GCACATATCCCACTATCTCTCGCAAGCCCTTCCCTCTATATAAGGAAGTTCATTTCAATTCG	717		
DB	544	GCACATATCCCACTATCTCTCGCAAGNNCTTCTCTATATAAGGAAGTTCATTTCAATTCG	603		
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CK438362

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DEFINITION Q00083.BR_J24 Q0008: Cambium, phloem and bark of girdled saplings
Picea glauca cDNA clone Q00083 J24 5', mRNA sequence

ACCESSION CK438362

VERSION CK438362.1 GI:40769522

KEYWORDS EST.

SOURCE Picea gl.

ORGANISM *Picea glauca*

Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.

REFERENCE 1 (bases 1 to 741)

AUTHORS
Morency, M.-J., Cook

Retzel, E., Butterfield, Y., Barber, S., Yang, G., Stott, J.,

Siddiqui, A., Holt, R., Marra, M. and MacKay, J.

TITLE	JOURNAL	COMMENT
1. The Role of the Teacher in the Classroom	Journal of Educational Research	1980, Vol. 83, No. 1, pp. 1-10
2. The Impact of Technology on Education	Journal of Educational Research	1980, Vol. 83, No. 2, pp. 11-20
3. The Importance of Parental Involvement	Journal of Educational Research	1980, Vol. 83, No. 3, pp. 21-30
4. The Effect of Teacher Expectations on Student Achievement	Journal of Educational Research	1980, Vol. 83, No. 4, pp. 31-40
5. The Role of the School in the Community	Journal of Educational Research	1980, Vol. 83, No. 5, pp. 41-50
6. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	1980, Vol. 83, No. 6, pp. 51-60
7. The Importance of Teacher Evaluation	Journal of Educational Research	1980, Vol. 83, No. 7, pp. 61-70
8. The Effect of Teacher Salary on Student Achievement	Journal of Educational Research	1980, Vol. 83, No. 8, pp. 71-80
9. The Role of the School in the Community	Journal of Educational Research	1980, Vol. 83, No. 9, pp. 81-90
10. The Impact of Teacher Education on Student Achievement	Journal of Educational Research	1980, Vol. 83, No. 10, pp. 91-100

Arborea EST sequencing in *Picea glauca* (white spruce)
Unpublished (2004)
Contact: John Mackay
Centre de Recherche en Biologie Forestiere
Universite Laval
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Fax: 418 656 7493
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Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN id Identifier: MN5173771 Clone ID:
GQ0083.J24 Clones available through: John Mackay, Ph. D. Professeur
adjoint - Assistant professor EMAIL: jmackay@svs.ulaval.ca Centre
de Recherche en Biologie Forestiere (Forest Biology Research
Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
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Seq primer: M13 Reverse primer.

FEATURES
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of trees girdled by removing a ring of bark ca. 1 cm wide
from the midpoint of the main stem"
/dev_stage="Vascular cambium, secondary phloem, and bark
from trees harvested 1 and 7 days after girdling
treatment"
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/clone_lib="GQ008: Cambium, phloem and bark of girdled
saplings"
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approximately 60 cm tall; Vector: pBluescript II SK (+)
XR; Site 1: Eco-RI; Site 2: Xho-I; Tissues were pooled
from above and below the girdle. cDNA was prepared from 5
mg of poly A+ selected RNA and was directionally ligated
into the pBluescript II SK (+) XR vector (Stratagene),
transformed by electroporation into DH10B cells (in
vitrogen) for propagation"

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ORIGIN

	Query Match	74.0%; Score 544..6; DB 7; Length 741;
	Best Local Similarity 94.4%; Pred. No. 7..9e-160;	
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Qy 598 CCAACACAGCTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAAGGATGAC 657

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Db 577 GCACAAATCCCACTATCTTCGCAAGACCTTCCTCTATATAAGAAAGTTCATTTCATTG 636

Qy 718 GAGAGGACA 726

Db 637 GAGAGGAGA 645

RESULT 7

CK437920

LOCUS

DEFINITION

GQ0081_BR_F05 GQ008: Cambium, phloem and bark of girdled saplings

Picea glauca cDNA clone GQ0081_F05 5', mRNA sequence.

CK437920

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Picea glauca (white spruce)

Picea glauca

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.

1 (bases 1 to 655)

Morency, M.-J., Cooke, J., Pavy, N., Parsons, L., Paule, C., Seguin, A., Retzel, E., Butterfield, Y., Barber, S., Yang, G., Stott, J., Siddiqui, A., Holt, R., Marra, M. and Mackay, J.

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Unpublished (2004)

Contact: John Mackay

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Universite Laval

Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4

Fax: 418 656 7493

Email: jmackay@svs.ulaval.ca

Center for Computational Genomics and Bioinformatics (CCGB), University of Minnesota, MN id Identifier: MN5171736 Clone ID: GQ0081_F05 Clones available through: John Mackay, Ph. D. Professeur adjoint - Assistant professor EMAIL: jmackay@svs.ulaval.ca Centre de Recherche en Biologie Forestiere (Forest Biology Research Center) Universite Laval Quebec, Quebec CANADA G1K 7P4

Plate: 1 row: 05 column: F

Seq primer: M13 Reverse Primer.

FEATURES

Location/Qualifiers

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/lab_host="E. coli DH10B cells"

/clone_lib="GQ008: Cambium, phloem and bark of girdled saplings"

/notes="Organ: Main stem of 4 year old saplings, approximately 60 cm tall; Vector: pBluescript II SK (+) XR; Site_1: EcoRI; Site_2: Xho-I; Tissues were pooled from above and below the girdle. cDNA was prepared from 5 mg of poly A+ selected RNA and was directionally ligated

into the pBluescript II SK (+) XR vector (Stratagene), transformed by electroporation into DH10B cells (in vitrogen) for propagation"

ORIGIN

Query Match 73.0%; Score 537.2; DB 7; Length 655;

Best Local Similarity 92.5%; Pred. No. 1.6e-157;

Matches 567; Conservative 0; Mismatches 43; Indels 3; Gaps 1;

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Db 144 TCGATATAAGGAAAGGCTATCGTTGAAGATGCCCTCTGCCGACACAGTGGTCCCAAGATGGA 203

Qy 301 CCCCACCCACGAGGAGCATCGTGGAAAAGAGAGCTTCCACACGCTCTTCAAAAGCAA 360

Db 204 CCCCACCCACGAGGAGCATCGTGGAAAAGAGAGCTTCCACACGCTCTTCAAAAGCAA 263

Qy 361 GTGGATTGATGTGATTG---CAGTGAAGACTTTTCAACAAAGGTAATATCGGAAAACCTC 417

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Db 384 GGCCTCTACAAATGCCATCATTCGCGATAAGGAAAGGCTATCGTTCAAGATGCTCTGCC 443

Qy 538 GACAGTGGTCCCAAGATGGACCCCCACGAGGAGCATCGTGAAAAGAAAGACGTT 597

Db 444 GACAGTGGTCCCAAGATGGACCCCCACGAGGAGCATCGTGAAAAGAAAGACGTT 503

Qy 598 CCAACACAGCTTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAAGGATGAC 657

Db 504 CCAACACAGCTTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAAGGATGAC 563

Qy 658 GCACATCCCACTATCTTCGCAAGACCTCTCTCTATATAAGAAAGTTCATTTCATTG 717

Db 564 GCACATCCCACTATCTTCGCAAGACCTCTCTCTATATAAGAAAGTTCATTTCATTG 623

Qy 718 GAGAGGACACGCT 730

Db 624 GAGANNNNNNNT 636

RESULT 8

CK438485

LOCUS

DEFINITION

GQ0085_BR_M24 GQ008: Cambium, phloem and bark of girdled saplings

Picea glauca cDNA clone GQ0085_M24 5', mRNA sequence.

CK438485

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Picea glauca (white spruce)

Picea glauca

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.

1 (bases 1 to 736)

Morency, M.-J., Cooke, J., Pavy, N., Parsons, L., Paule, C., Seguin, A., Retzel, E., Butterfield, Y., Barber, S., Yang, G., Stott, J., Siddiqui, A., Holt, R., Marra, M. and Mackay, J.

Arborea EST sequencing in Picea glauca (white spruce)

Unpublished (2004)

Contact: John Mackay

Centre de Recherche en Biologie Forestiere
Universite Laval
Pavillon Charles-Eugene Marchand, Quebec, Canada G1K 7P4
Fax: 418 656 7493
Email: jmackay@rsvs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN id Identifier: MN5174611 Clone ID:
GQ0085 M24 Clones available through: John Mackay, Ph. D. Professeur
adjoind -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
de Recherche en Biologie Forestiere (Forest Biology Research
Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
Plate: 5 row: 24 column: M
Seq primer: M13 Reverse Primer.

FEATURES source

Location/Qualifiers
1. 736
/organism="Picea glauca"
/mol_type="mRNA"
/strain="pg-653"
/db_xref="taxon:3330"
/clone="GQ0085 M24"
/sex="Hermaphrodite"
/tissue_type="Vascular cambium, secondary phloem and bark
of trees girdled by removing a ring of bark ca. 1 cm wide
from the midpoint of the main stem"
/dev_stage="Vascular cambium, secondary phloem, and bark
from trees harvested 1 and 7 days after girdling
treatment"
/lab_host="E. coli DH10B cells"
/clone_lib="GQ008: Cambium, phloem and bark of girdled
saplings"
/note="Organ: Main stem of 4 year old saplings,
approximately 60 cm tall; Vector: pBluescript II SK (+)
XR; Site 1: Eco-RI; Site 2: Xho-I; Tissues were pooled
from above and below the girdle. cDNA was prepared from 5
mg of poly A+ selected RNA and was directionally ligated
into the pBluescript II SK (+) XR vector (Stratagene),
transformed by electroporation into DH10B cells (in
vitrogen) for propagation"

ORIGIN

Query Match 72.4%; Score 535.2; DB 7; Length 736;
Best Local Similarity 94.8%; Pred. No. 7.1e-157;
Matches 565; Conservative 0; Mismatches 28; Indels 3; Gaps 1;
Qy 121 AGTGAGACTTTTCAACAAAGGTTAATTCGGGAAACCTCTCGGATTCATTCGCCAGCT 180
Db 40 ATTGAGACTTTTCAACAAAGGTTAATTCGGGAAACCTCTCGGATTCATTCGCCAGCT 99
Qy 181 ATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCCATCAT 240
Db 100 ATCTGTCACTTTATTGTGAAGATAGTGAAAAGGAAGGTGGCTCTCTACAAATGCCATCAT 159
Qy 241 TGCATTAAGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAGATGGA 300
Db 160 TGCATTAAGAAAGGCGCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAGATGGA 219
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Db 220 CCCCACCCAGGAGCATCGTGAAAAGGAAGACAGCTTCCACACAGCTCTTCAAGACAA 279
Qy 361 GTGGATTGATGTATTG---CAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTC 417
Db 280 GTGGATTGATGTATTGTCGGATTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTC 339
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Db 340 CTCGGATTCCATTCGCCAGCTATCTGTCACTTTCATTTATTGTGAAGATAGTGGAAAAGGAAGGT 399
Qy 478 GGCACCTTCAAAATGCATTCATTGCGATAAAGGAAGGCTATCGTTTCAAGATGCCTCTGCC 537
Db 400 GGCCTTCAAAATGCCATTCATTGCGATAAAGGAAGGCGCATCGTTTGAAGATGCCTCTGCC 459
Qy 538 GACAGTGGTCCCAAGATGGACCCCCACCCAGGAGGACATCGTGGAAAAAGGAAGACGTT 597

Db 460 GACAGTGGTCCCAAGATGGACCCCCACCCAGGAGGACATCGTGGAAAAAGGAAGCGTT 519
Qy 598 CCACACAGCTCTTCAAGCAAGTGGATTGTATGTATCTCCACTGACGTAAAGGATGAC 657
Db 520 CCACACAGCTCTTCAAGCAAGTGGATTGTATGTATCTCCACTGACGTAAAGGATGAC 579
Qy 658 GCACAAATCCCACTATCTTCGCAAGACCCCTCTCTATATAAGGAAGTTCATTTC 713
Db 580 GCACAAATCCCACTATCTTCGCAAGACCCCTCTCTATATAAGGAAGTTCATTTC 635

RESULT 9

CK438348
LOCUS
DEFINITION
GQ0085.BR.D16.GQ008: Cambium, phloem and bark of girdled saplings
Picea glauca cDNA clone GQ0085.D16.5', mRNA sequence.
CK438348
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Picea glauca (white spruce)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
REFERENCE
AUTHORS
Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A.,
Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J.,
Siddiqui,A., Holt,R., Marra,M. and Mackay,J.
Arborea EST sequencing in Picea glauca (white spruce)
Unpublished (2004)
COMMENT
Contact: John Mackay
Centre de Recherche en Biologie Forestiere
Universite Laval
Pavillon Charles-Eugene Marchand, Quebec, Canada G1K 7P4
Fax: 418 656 7493
Email: jmackay@rsvs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN id Identifier: MN5174387 Clone ID:
GQ0085 D16 Clones available through: John Mackay, Ph. D. Professeur
adjoind -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
de Recherche en Biologie Forestiere (Forest Biology Research
Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
Plate: 5 row: 16 column: D
Seq primer: M13 Reverse Primer.

FEATURES source

Location/Qualifiers
1. 698
/organism="Picea glauca"
/mol_type="mRNA"
/strain="pg-653"
/db_xref="taxon:3330"
/clone="GQ0085 D16"
/sex="Hermaphrodite"
/tissue_type="Vascular cambium, secondary phloem and bark
of trees girdled by removing a ring of bark ca. 1 cm wide
from the midpoint of the main stem"
/dev_stage="Vascular cambium, secondary phloem, and bark
from trees harvested 1 and 7 days after girdling
treatment"
/lab_host="E. coli DH10B cells"
/clone_lib="GQ008: Cambium, phloem and bark of girdled
saplings"
/note="Organ: Main stem of 4 year old saplings,
approximately 60 cm tall; Vector: pBluescript II SK (+)
XR; Site 1: Eco-RI; Site 2: Xho-I; Tissues were pooled
from above and below the girdle. cDNA was prepared from 5
mg of poly A+ selected RNA and was directionally ligated
into the pBluescript II SK (+) XR vector (Stratagene),
transformed by electroporation into DH10B cells (in
vitrogen) for propagation"

ORIGIN

Query Match 72.4%; Score 533.2; DB 7; Length 698;
Best Local Similarity 94.5%; Pred. No. 3e-156;

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QY	121	AGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTCGCCAGCT	180						
Db	37	ATTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTCGCCAGCT	96						
QY	181	ATCTGTCACTTCATCAAAAGGACAGTAGAAAAAGGAGGTGGACCTTACAAATGCCATCAT	240						
Db	97	ATCTGTCACTTTATTGTGAAGATAGTGGAAAGAGGTGGCTCTCTACAAATGCCATCAT	156						
QY	241	TGCGATAAAGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAGATGGA	300						
Db	157	TGCGATAAAGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCCAAAGATGGA	216						
QY	301	CCCCACCCAGGAGGACATCGTGGAAAAAGAGAGCGTTCCACACGCTTTCAAAGCAA	360						
Db	217	CCCCACCCAGGAGGACATCGTGGAAAAAGAGAGCGTTCCACACGCTTTCAAAGCAA	276						
QY	361	GTGGATTGATGTATTG--CAGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTC	417						
Db	277	GTGGATTGATGTATTGTCGATTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTC	336						
QY	418	CTCGGATTCATTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAAGGAGGT	477						
Db	337	CTCGGATTCATTGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAGGAGGT	396						
QY	478	GGCACTTACAAATGCCATCATTCGGATAAAGGAGGCTATCTTCAAGATGCTCTGCC	537						
Db	397	GGCTCTTACAAATGCCATCATTCGGATAAAGGAGGCTATCTTCAAGATGCTCTGCC	456						
QY	538	GACAGTGGTCCCAAGATGACCCCAACGAGGAGCATCGTGGAAAAAGGAGGAGT	597						
Db	457	GACAGTGGTCCCAAGATGACCCCAACGAGGAGCATCGTGGAAAAAGGAGGAGT	516						
QY	598	CCAAACCAAGTTCCTTCAAGCAAGTGGATTGATGATATCTCCACTGACGTAAGGATGAC	657						
Db	517	CCAAACCAAGTTCCTTCAAGCAAGTGGATTGATGATATCTCCACTGACGTAAGGATGAC	576						
QY	658	GCACATCCCACTATCTTCCGAGACCTCTCTATATAAGGAAGTTCATTCA	713						
Db	577	GCACATCCCACTATCTTCCGAGANNCTCTCTATATAAGGAAGTTCATTCA	632						

RESULT 10
CO481168
LOCUS
DEFINITION
Picea glauca cDNA clone GQ0165_M24 3', mRNA sequence.
CO481168
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Picea glauca (white spruce)
Picea glauca
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
1 (bases 1 to 610)
Morency, M.-J., Cooke, J., Pavy, N., Parsons, L., Paule, C., Seguin, A.,
Retzel, E., Butterfield, Y., Barber, S., Yang, G., Scott, J.,
Siddiqui, A., Holt, R., Marra, M. and Mackay, J.
Arborea EST sequencing in Picea glauca (white spruce)
Unpublished (2004)
Contact: John Mackay
Centre de Recherche en Biologie Forestiere
Universite Laval
Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4
Fax: 418 656 7493
Email: jmackay@rsvs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN id Identifier: MN5268594 Clone ID:
GQ0165_M24 Clones available through: John Mackay, Ph. D. Professeur
adjoint - Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
de Recherche en Biologie Forestiere (Forest Biology Research
Center) Universite Laval Quebec, Quebec CANADA G1K 7P4

FEATURES	source	Plate: 5	row: 24	column: M	Seq primer: T7 Primer.	Location/Qualifiers
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						/clone="GQ0165_M24"
						/sex="Hermaphrodite"
						/tissue_type="Xylem, pith, cambium, phloem, bark"
						/dev_stage="Primary & secondary shoot, secondary phloem
						pooled from plants fertilized with low and high NH4NO3"
						/lab_host="E. coli DH10B cells"
						/clone_lib="GQ016: Primary, secondary SHOOT -N fertil.
						treatments"
						/note="Organ: Main stem region producing secondary growth
						on 60 cm tall seedlings; Vector: pBluescript II SK (+) XR;
						Site 1: Eco-RI; Site 2: Xho-I; cDNA was prepared from 5 mg
						of poly A+ selected RNA and was directionally ligated into
						the pBluescript II SK (+) XR vector (Stratagene),
						transformed by electroporation into DH10B cells (in
						vitrogen) for propagation"
ORIGIN						
		Query Match	65.3%;	Score 480.8;	DB 7;	Length 610;
		Best Local Similarity	93.6%;	Pred. No. 9e-140;		
		Matches 510;	Conservative 0;	Mismatches 32;	Indels 3;	Gaps 1;
QY	185	GTCACTTTCATCAAAAGGACAGTAGAAAAAGGAGGTGGACCTTCAAAATGCCATTCATTCGC	244			
Db	1	GTCACTTTATTGTGAAGATAGTGGAAAAAGNNNGCTCTTACAAATGCCATTCATTCGC	60			
QY	245	ATAAGGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCAAAGATGGACCCC	304			
Db	61	ATAAGGAAAGGCTATCGTTCAAGATGCTCTGCCGACAGTGGTCCAAAGATGGACCCC	120			
QY	305	CACCCACGAGGAGCATCGTGGAAAAAGAGCGTTCCAAACCGCTCTTCAAAGCAAGTGG	364			
Db	121	CACCCACGAGGAGCATCGTGGAAAAAGAGCGTTCCAAACCGCTCTTCAAAGCAAGTGG	180			
QY	365	ATTGATGTGATTG--CAGTGAGACTTTTCAACAAAGGGTAAATATCGGAAACCTCTCTCG	421			
Db	181	ATTGATGTGATGTCGCTCGATTGAGACTTTTCAACAAAGGGTAAATATCGGAAACCTCTCTCG	240			
QY	422	GATTCATTGCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAGGAGGTGGCA	481			
Db	241	GATTCATTGCCAGCTATCTGTCACTTTCATCAAAAGGACAGTAGAAAAAGGAGGTGGCT	300			
QY	482	CCTACAAATGCCATCATTCGATATAAGGAAAGGCTATCGTTCAAGATGCTCTTGGCGACA	541			
Db	301	CCTACAAATGCCATCATTCGATATAAGGAAAGGCTATCGTTCAAGATGCTCTTGGCGACA	360			
QY	542	GTGGTCCCAAGATGGACCCCAACCGAGGAGCATTCGTGGAAAAAGAGAGCTTCCAA	601			
Db	361	GTGGTCCCAAGATGGACCCCAACCGAGGAGCATTCGTGGAAAAAGAGAGCTTCCAA	420			
QY	602	CCACGCTTCAAAGCAAGTGGATTGATGTCATATCTCCACTGACGTAAGGATGACGCAC	661			
Db	421	CCACGCTTCAAAGCAAGTGGATTGATGTCATATCTCCACTGACGTAAGGATGACGCAC	480			
QY	662	AATCCCACTATCTCTCGCAAGACCTTCTCTATATAAGGAAGTTCATTTTCATTTGGAGA	721			
Db	481	AATCCCACTATCTCTCGCAAGACCTTCTCTATATAAGGAAGTTCATTTTCATTTGGAGA	540			
QY	722	GGACA 726				
Db	541	GGAGA 545				
		839 bp	DNA	linear	GSS	03-FEB-1999
		AQ362115				
		LOCUS				
		RESULT 11				
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		LOCUS				

DEFINITION mgxb0003F18f CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0003F18f, genomic survey sequence.
 ACCESSION AQ362115
 VERSION AQ362115.1 GI:4211034
 KEYWORDS GSS.
 SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
 ORGANISM Magnaporthe grisea
 REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. 1 (bases 1 to 839)
 AUTHORS Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
 TITLE A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Genome
 JOURNAL Unpublished (1998)
 COMMENT Contact: Dean RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 4293
 Email: rdean@clemson.edu
 Seq primer: TAATACGACTCACTATAGG
 Class: BAC ends
 High quality sequence start: 58
 High quality sequence stop: 454.
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 /clone="mgxb0003F18f"
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 /lab_host="E. coli DH108"
 /clone_lib="CUGI Rice Blast BAC Library"
 /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII; Rice blast is one of the most devastating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."
 FEATURES
 source

ORIGIN

Query Match 47.8%; Score 351.8; DB 8; Length 839;
 Best Local Similarity 99.4%; Pred. No. 4.1e-99;
 Matches 353; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 Db 163 ATTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTCGCCAGCT 222
 Qy 439 ATCTGTCACTTCATCAAAAGGACAGTAGAAAGGAGGTGGCAGCTCAAAATGCCATCAT 498
 Db 223 ATCTGTCACTTCATCAAAAGGACAGTAGAAAGGAGGTGGCAGCTCAAAATGCCATCAT 282
 Qy 499 TGGGATAAAGAAAGGCTATCGTTCAAGATCGCTCTCGCGACAGTGGTCCCAAGATGGA 558
 Db 283 TGGGATAAAGAAAGGCTATCGTTCAAGATCGCTCTCGCGACAGTGGTCCCAAGATGGA 342
 Qy 559 CCCCCACCCAGGAGGATCGTGGAAAAGAGAGCGTTTCAACAGCTCTTCAAGCAA 618
 Db 343 CCCCCACCCAGGAGGATCGTGGAAAAGAGAGCGTTTCAACAGCTCTTCAAGCAA 402
 Qy 619 GTGGATTGATGTGATATCTCCACTGACGTGAAGGATGACGACAAATCCCACTATCCTTCG 678
 Db 403 GTGGATTGATGTGATATCTCCACTGACGTGAAGGATGACGACAAATCCCACTATCCTTCG 462

Qy 679 CAAGACCCCTTCTCTATATTAAGGAAGTTTCATTTTCATTTGGAGAGACACGCTGGA 733
 Db 463 CAAGACCCCTTCTCTATATTAAGGAAGTTTCATTTTCATTTGGAGAGACACGCTGGA 517
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 CG206846/c
 LOCUS
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 ACCESSION CG206846
 VERSION CG206846.1 GI:34097907
 KEYWORDS GSS.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza. 1 (bases 1 to 654)
 AUTHORS Li, Y., Wu, C., Santos, T., Uhm, T., Liu, D. and Zhang, H.-B.
 TITLE BAC end sequences to close the gaps of a rice physical map at TAMU
 JOURNAL Unpublished (2003)
 COMMENT Contact: Wu C
 Department of Soil and Crop Sciences and Institute for Plant Genomics and Biotechnology
 Texas A & M University
 TAMU 2474, College Station, TX 77843-2474, USA
 Tel: 979 862 4800
 Fax: 979 862 4790
 Email: c-wu@neo.tamu.edu
 Seq primer: M13 universal Forward GTAAACACGCGCCAGT
 Class: BAC ends
 High quality sequence stop: 654.
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 /clone="TOSJNH019110h"
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 /lab_host="E. coli DH108"
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 /note="Vector: V41"
 ORIGIN

ORIGIN

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 Matches 347; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 Qy 379 AGTGAGACTTTTCAACAAAGGGTAATATCGGAAACCTCTCGGATTCATTCGCCAGCT 438
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 Db 464 ATCTGTCACTTCATCGAAAGGACAGTAGAAAGGAGGTGGCTCTCAAAATGCCATCAT 405
 Qy 499 TGGGATAAAGAAAGGCTATCGTTCAAGATCGCTCTCGCGACAGTGGTCCCAAGATGGA 558
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 Qy 619 GTGGATTGATGTGATATCTCCACTGACGTGAAGGATGACGACAAATCCCACTATCCTTCG 678
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 Qy 679 CAAGACCCCTTCTCTATATTAAGGAAGTTTCATTTTCATTTGGAGAGACACGCTGGA 735

Db	331	ATCTGTCTCTTATTGTGGAAGATAGTGGAAAAGGAAGTGGCTCTCTCAAAATGCCATCAT	272
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Qy	559	CCCCACCCACGAGGAGCATCGTGGAAAAAGAACGTTCCAAACCAAGCTCTTCAAAGCAA	618
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Db	151	GTGGATTGATGTGATATCTCCACTGACGTAAAGGATGACGCACAATCCCACTATCCTTCG	92
Qy	679	CAAGACCCCTTCTCTATATAAGGAAGTTCATTTCAATTTGGAGAGGACACGCTGGA	733
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RESULT 15	
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LOCUS	469 bp DNA linear GSS 10-NOV-2003
DEFINITION	1118056A07.y1 1118 - RescueMu Grid S Zea mays genomic, genomic survey sequence.
ACCESSION	CG804983
VERSION	CG804983
KEYWORDS	CG804983.1 GI:38240957
SOURCE	GSS.
ORGANISM	Zea mays
	Zea mays
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE	1 (bases 1 to 469)

ORIGIN

Query Match 45.2%; Score 332.6; DB 9; Length 469;

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Best Local Similarity 96.1%; Pred. No. 3.7e-93;
Matches 341; Conservative 0; Mismatches 14; Indels 0; Gaps 0

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QY 439 ATCTGTGCATTTTCATCAAAAGGACAGTAGAGAAAGGAAGGTGGCCACTACAAATGCCATCAT 498
Db 330 ATCTGTGCATTTTATTGTGAAGATAGTGGAAAGGAAGGTGGCTCTCTACAAATGCCATCAT 271
QY 499 TGCGATTAAGGAAAGGCTATTCGTTCAAGATGCCTCTGCGGACAGTGGTCCCAAAGATGGA 558
Db 270 TGCGATTAAGGAAAGGCGCATCGTTGAAGATGCCTCTGCGGACAGTGGTCCCAAAGATGGA 211
QY 559 CCCCCACCCACGAGGAGCATCGTGGAAAGAAAGAACAGCTTCCAAACCAGCTCTTCAAAGCAA 618
Db 210 CCCCCACCCACGAGGAGCATCGTGGAAAGAAAGAACAGCTTCCAAACCAGCTCTTCAAAGCAA 151
QY 619 GTGGATTGATGTGTGATATCTCCACATGACGTAAAGGATGACGCACAATCCCACTATCTCTTCG 678
Db 150 GTGGATTGATGTGTGATATCTCCACATGACGTAAAGGATGACGCACAATCCCACTATCTCTTCG 91
QY 679 CAAGACCCCTTCTCTATATAGGAAGTTTCATTTCTGGAGAGGACACGCTGGA 733
Db 90 CAAGACCCCTTCTCTATATAGGAAGTTTCATTTCTGGAGAGGACACGCTGGA 36

Search completed: October 11, 2005, 18:59:18
Job time : 3219 secs

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